

# STIC Search Report Biotech-Chem Library

#### STIC Database the control of the con

TO: Ruixiang Li

Location: REM/4D75/4C70

Art Unit: 1646

Friday, November 25, 2005

Case Serial Number: 09/475158

From: Toby Port

**Location: Biotech-Chem Library** 

**REM-1A59** 

Phone: 571-272-2523

toby.port@uspto.gov

#### Searcia Noiss

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port X22523



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From:

Li, Ruixiang

Sent:

Monday, October 31, 2005 2:39 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search of Application No.09/475,158

Please do a standard search on:

- (i).SEQ ID NOS: 3 and 5 against both commercial and interference amino acid databases;
- (ii). SEQ ID NOS: 14, 15, and 16 against both commercial and interference nucleic acid databases;
- (iii). AlaValSerGlulleGlnLeuMetHisAsnLeuGlyGlyGlyGlyGly against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li GAU 1646 REM 4D75 Mail Box 4C70 (571) 272-0875

OCT 31 2005

""ECH/CHEM DIVISION
(STIC)

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#\_\_\_\_\_ AA#:\_\_\_

S/L:\_\_\_\_ Oligomer:\_\_\_\_

Encode/Transl:\_\_\_\_

Structure #:\_\_\_\_ Text:\_\_

Inventor:\_\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*
Vendors and cost where applicable
STN:\_\_\_\_\_
DIALOG:\_\_\_\_
QUESTEL/ORBIT:\_\_\_\_
LEXIS/NEXIS:\_\_\_\_
SEQUENCE SYSTEM:\_\_\_\_
WWW/Internet:\_\_\_\_
Other (Specify):\_\_\_\_\_

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[Ala14]-h [Ala13]-h [Ala1, Ile [Ser14]-h [Ash113]-h [Ash113]-h [Ala14]-h [Ala14]-h Amino aci Amino aci Human par Human par

Aar58209
Aar58207
Aar58021
Aar58031
Aar58093
Aar58103
Aar58103
Aar58108
Aar58108
Aar82202
Aaw42059
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Human par Human par

Human par Parathyro N-termina

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OM protein

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Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                       PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tetherl; osteoporosis.
                                                                                                                                                                                                                                                                         Parathyroid hormone functional domain conjugate peptide PG5
                                                                                                                                                                                                                                                                                                                                              /label= PTH C-terminal binding portion 'note= "residues 15-31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
                                                                                                                                                                                    ALIGNMENTS
       ADÇ75489
AAR58209
AAR58209
AAR58024
AAR58024
AAR58033
AAR58039
AAR58039
AAR58103
AAR58103
AAR58095
AAW8108
AAR58095
AAW42059
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                          AAY96973 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                      10. .14
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US031108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0114577P
                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      15. .30
/label=
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-452384/39.
N-PSDB; AAA51729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTTS J T.
JUEPPNER H.
                                                                               888888
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200039278-A2
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                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                          Synthetic
AAY96973;
                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRON/)
                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUEP/)
                                                                                                                                                                                                                    AAY96973
 Aay66975 Parathyro
Aar28104 [G1y13]-h
Aar22294 Human par
Aar58071 [Ala11]-h
Aay6015 Human ami
Aay98014 Human ami
Aay98014 Human ami
Aar58026 Nalpha-m
Aar58026 [Ala1]-hP
Aar58026 [Ala1]-hP
Aar58019 Nalpha-m
Aar58019 Nalpha-m
Aar2206 Human par
Aay6674 Parathyro
Aar2206 Human par
Aay6574 Parathyro
Aar3029 Parathyro
                                                                                                                                                                                                                                                                                                                                                                                               Aay96973 Parathyro
                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      ; Search time 141.5 Seconds (without alignments) 96.260 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                             2443163
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                      31
                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                     1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
                                                                                                                                              2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                       November 21, 2005, 15:52:37
                                                                                                                                                                                                   Minimum Mátch 0%
Maximum Match 100%
Listing first 45 summaries
                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY98014
AAR58248
AAR58026
AAR58019
AAY96974
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AAY3030
AAW03130
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AAU73173
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AAR22294
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AAY96975
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geneseqp2000s: *
geneseqp2001s: *
geneseqp2001s: *
geneseqp2003as: *
geneseqp2003bs: *
geneseqp2004s: *
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length: 2000000000
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                                                                                                                      BLOSUM62
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Match
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sed
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RESULT 3
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                                                     Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. Si as an amino terminal signaling functional domain of parathyroid hormone (PTH); Lis a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-134) or a PTH-retack protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor che new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling treating diseases in a mammalian call having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large mative PTH or PTHTP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid hormone functional domain conjugate peptide PG7.
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 160; DB 3; Length 31; 100.0%; Pred. No. 1.4e-14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .9
/label= PTH N-terminal_signaling_domain
/note= "resīdues 1-9"
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/label= PTH C-terminal_binding_portion
/note= "residues 17-31"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                        Claim 7; Page 92-93; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96975 standard; peptide; 31 AA
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/label= linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100. es 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GARD/) GARDELLA T J. (KRON/) KRONENBERG H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-452384/39.
N-PSDB; AAA51730.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 31 AA;
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Synthetic.
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AAY96975

XX AAY96775

XX AAY97

XX AAY97

XX PTH;

XW PTH;

XW PTH;

XW PTH;

XW PCOOL

XX COOL

XX 
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Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. Sis an amino terminal signaling functional domain of parathyroid hormone (PTH); Lis a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(-1,34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence: The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis
New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 91.2%; Score 146; DB 3; Length 31; Local Similarity 93.5%; Pred. No. 1.2e-12; nes 29; Conservative 0; Mismatches 2; Indels
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                                                                                                                           Claim 7; Page 93; 119pp; English
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92GB-00026859.
92GB-00026861.
93GB-0001691.
93GB-0001692.
93GB-00007673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [Gly13]-hPTH(1-38)-OH.
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23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APR-1993;
19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1994.
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Matches
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AAR74462 standard; peptide; 35 AA.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                  and vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                     25-MAR-2003
                                              01-DEC-1995
                                                                                                                                   Synthetic
                   AAR74462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide(s) are parathyroid hormone derivs. - used in hormone therapy, for treating osteoporosis hyperparathyroidism and hypertension.
                                                                                                                                                                                                                                                                       hPTH; protease resistant; osteoporosis; hypoparathyroidism; hypertension.
This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The peptide is an analogue of human parathyroid hormone fragment 1-34. The peptide modification defined increase resistance to proteases and therefore persistance in the blood. The peptide is used in therapy of osteoporosis, hypoparathyroidism and hypertension. The peptide may be synthesised by the Merrifield solid phase method in an automatic apparatus. See also AAR22290-99. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                            Length 38;
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                                                                                              3; Indels
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Pred. No. 2.8e-10;
                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                    Ĥ
                                                                          Score 133; DB 2;
Pred. No. 9e-11;
1; Mismatches
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                                                                                                                 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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                                                                                                                                                                                                                                                    Human parathyroid hormone 1-34 [Ser 11]
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                                                                                                                                                                                    ¥.
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                                                                            83.1%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                     90JP-00257490.
                                                                                                                                                                                                                                                                                                                                                  91EP-00116303
                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                   (first entry)
                                                                          Query Match
Best Local Similarity 87.1:
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Fukuda T,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-106285/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                       hypoparathyroidism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34 AA;
                                                          Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1990;
06-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                   25-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa S,
                                                                                                                                                                                                                         25-MAR-2003
03-AUG-1992
                                                                                                                                                                                                                                                                                                                                01-APR-1992.
                                                                                                                                                                                                                                                                                                            EP477885-A.
                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                       AAR22294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   field.)
                                                                                                                                                                            AAR22294
                                                                                                                                                                 RESULT
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RESULT 5

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                                                                                                                                               Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution; osteoporosis; hypercalcaemia; hyperparathroidism; metabolic bone disease; human; veterinary medicine; iontophoretic transdermal transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New active analogues of parathyroid hormone - with increased activity, stability in serum etc., esp. for treating osteoporosis, also related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR74429-520 represent analogues of the 34 amino acid sequence of truncated human parathyroid hormone (PTH). These manalogues have increased activity and longer serum half life than native PTH due to eg. substitution of Met residues with Leu residues and replacing the carboxy Phe with Tyr. The carboxy terminal may also be modified by the addition of a homoserine residue or analogue, or by the addition of residues 35-84 of wild type PTH (see AAR74410). These PTH analogues may be used in the treatment of osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic bone diseases in human or account of the second of the second or analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Homoserine (Hse), Hse lactone, Hse amide or residues 35-84 of PTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.6%; Score 129; DB 2; I
80.6%; Pred. No. 2.9e-10;
ive 3; Mismatches 3;
                                                                                             Parathyroid hormone peptide analogue, Glyll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVSEIQLLHNGGKHLNSLERVEWLRKKLQDV
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 76; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= -H, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR58271 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US012205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00142551
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selick HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-178880/23.
                                                                                                                                                                                                                                                              recombinant E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR58271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
AAR58271
ID AAR5
XX
AC AAR5
XX
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parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the amino terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. The present sequence is a human PTH peptide, with an amino-terminal modification which results in effective activation of the PTH-2 receptor and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of hypercalcaemia. In turn, hypercalcaemia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers: breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and cesophagus. This peptide would be suitable for prophylaxis and treatment of the above fracture repair. The present sequence would be suitable for residue at position 1
                                                                                                                                                                                                                                                                                                                                                          New parathyroid hormone (PTH) analogs having one or more amino acid substitutions that confer PTH-1/PTH-2 receptor agonist properties, to treating old age osteoporosis and post-menopausal osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human parathyroid hormone analogue [Chall]hPTH(1-34)NH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= OTHER
/note= "Cyclohexylalanine (Cha)"
                                   /note= "Ala is desamino residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Bo. 0%; Score 128; DB 3;

Best Local Similarity 87.1%; Pred. No. 3.8e-10;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                       Bringhurst FR, Takasu H, Gardella TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW17941 standard; peptide; 34
                                                                                                                                            99WO-US027656.
                                                                                                                                                                                98US-0110152P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                    (BRIN/) BRINGHURST F R.
                                                                                                                                                                                                                                     TAKASU H.
GARDELLA T J.
                                                                                                                                                                                                                                                                                                                         WPI; 2000-400045/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33 AA;
                                                                       WO200031137-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                              23-NOV-1999;
                                                                                                                                                                              25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1997
                                                                                                             02-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW17941;
                                                                                                                                                                                                                                     (TAKA/)
(GARD/)
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  ###X#X#X#X#X####X#X####X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid hormone peptide; PTH; renal cell; osseous cell; human; signal transduction; osteoporosis; amino-terminal modification; bone disease; parathyroid hormone receptor; osteopannia; hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where talcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                                         Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human amino-terminal modified parathyroid hormone analogue # 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 129; DB 2;
Pred. No. 3e-10;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waelchli R, Rainer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36
/note= "in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 269; Page 46; 92pp; English.
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY98015 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                                              92GB-00026415.
92GB-00026859.
92GB-00026861.
93GB-0001691.
93GB-0001692.
93GB-0001693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.9%;
Matches 26; Conservative 1
                                                                                                                                                                                                                                                                                                                                                92GB-00015009
                                                                                                                                                                                                                                                                                                              93GB-00014384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
    20-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis I, Schneider H,
                                       [Ala11] -hPTH (1-36) -NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-018352/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANO ) SANDOZ LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 AA;
                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                           15-JUL-1992;
18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APR-1993;
19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2000
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                                                                                                                                                                                                                                                                                                            12-JUL-1993;
                                                                                                                                                                                                                                         GB2269176-A.
                                                                                                                                                                                                                                                                          02-FEB-1994
                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY98015;
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Gaps

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The invention relates to peptides of formula (I) containing at least one acc (i.e. 1-amino-1-(3-9C cycloalkane)-carboxylic acid) residue.

Acc (i.e. 1-amino-1-(3-9C cycloalkane)-carboxylic acid) residue.

(R1) (R2) A1-A3-G1-A3-G1-A24-Arg-Lys-A2-A28-A29-A30-A31-A32-A33-A34-R3

A-18-A19-Arg-A21-A32-A23-A24-Arg-Lys-A28-A29-A30-A31-A32-A33-A34-R3

(I); where A1 = Ser, Ala or Dap; A3, A17 = Ser, Thr or Aib; A5, A7, A11,

(I); where A1 = Ser, Ana or Dap; A3, A17 = Ser, Thr or Aib; A2 = G1y,

CC A15 = Leu, Nle, Ile, Cha, beta - Nal, Trp, Pal, Acc, Phe or p-(X)-Phe; X =

CC Or Aib; A16 = Ser, An, A1a or Aib; A18 = Met, Nva, Leu, Val, Ile,

CC Or Aib; A16 = Ser, An, A10 or Aib; A18 = Met, Nva, Leu, Val, Ile,

CC G1U; A23 = Trp, Acc or Cha; A24 = G1u, Acc or Cha; A2 =

CC G1U; A23 = Trp, Acc or Cha; A29 = G1u, Acc or Cha; A2 =

CC Lys, Aib, Leu, hArg, G1n, Acc or Cha; A29 = G1u, Acc or Cha; A3 = As or is deleted; A3 = Phe, Tyr, Amp or Aib; or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or is deleted; A3 = His or is

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or Chay, A2 =

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or Chay, A2 =

CLys, A31 = Val, Leu, Nle, Acc or Cha, Or Chay, A3 = His or is

CC aparthyroid hormone-related protein (PTHP) . They stimulate bone growth

CC parathyroid hormone-related protein (PTHP) . They stimulate bone growth

CC parathyroid hormone-related protein (PTHP) . They stimulate bone growth deficiency, e.g. osteoporosis and bone fersures. They are

CC para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parathyroid hormone peptide; PTH; renal call; osseous cell; human; signal transduction; osteoporosis; amino-terminal modification; bone disease; parathyroid hormone receptor; osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
                                                                                                                                                                                                                                                               Parathyroid hormone analogue peptide compounds - used for stimulating bone growth, e.g. in treatment of bone fractures or osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human amino-terminal modified parathyroid hormone analogue # 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 128; DB 2;
Pred. No. 3.9e-10;
1; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVSEIQLMHNXGKHLNSMERVEWLRKKLQDV 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY98014 standard; peptide; 34 AA
                                              97US-00779768.
97US-00813534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.9%;
Matches 26; Conservative 1
97WO-US022498
                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000 (first entry)
                                                                                                                     (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                         WPI; 1998-399065/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34 AA;
  38-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                   07-JAN-1997;
                                                                          07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY98014;
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                                                                                                                                                                           Dong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is cyclohexylalanine (Cha). In this example the Leu residue at position 11 of the wild-type has been substituted by Cha. The hPTH analogues frimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and acalcitonin). N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parathyroid hormone; parathormone; bone growth; bone fracture; osteroporosis; anti-resorptive therapy; calcitonin.
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83.9%; Pred. No. 3.9e-10;
iive 1; Mismatches 4;
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       34
/note= "In amide form"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parathyroid hormone analogue #3.
                                                                                                                                                                           96WO-US011292
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96US-00626186.
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ses 26; Conservative
                                                                                                                                                                                                                                                                                                                        (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-118819/11.
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                                                                                                                                                                             03-JUL-1996;
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29-MAR-1996;
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Matches
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Gaps

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Length 34; 4; Indels

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/note= "N-alpha-methyl-Ala replaces wild-type Ser residue at position 1"
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                                                                                                        92GB-00015009.
92GB-00026859.
92GB-00026861.
93GB-0001691.
93GB-00001692.
93GB-00007673.
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Modified-site
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Modified-site
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28-JAN-1993;
14-APR-1993;
19-APR-1993;
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                                  GB2269176-A.
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                                                                                                                                                                                                                                                                                                                            Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the anino terminal is important for signal transduction. The present sequence is a human PTH speptide, with an amino-terminal modification which results in effective activation of the PTH-2 receptor and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osecoporosis, osteopeania, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers; breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oseophagus. This peptide would be suitable for prophylaxis and treatment of the above disorders. In addition, the present sequence would be suitable for residue at position 1
                                                                                                                                                                                                                                                         New parathyroid hormone (PTH) analogs having one or more amino acid substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful for treating old age osteoporosis and post-menopausal osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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                                    /note= "Ala is desamino residue"
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/note= "N-Dimethyl-Ala."
                                                                                                                                                                                                            Gardella TJ;
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             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              Claim 3; Page 63; 69pp; English.
                                                                                                            99WO-US027656.
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                                                                                                                                                                                                           Bringhurst FR, Takasu H,
                                                                                                                                                          (BRIN/) BRINGHURST F R.
(TAKA/) TAKASU H.
(GARD/) GARDELLA T J.
                                                                                                                                                                                                                                    WPI; 2000-400045/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34 AA;
                                                           WO200031137-A1
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Modified-site
              Key
Modified-site
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Matches
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XXX
AAC
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DDT 20-S
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FFT Modil
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This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
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36
/note= "in amide form"
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WPI; 1994-018352/03.
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Matches 27; Conserv
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                                                                                                                                                                                                                               Sequence 36 AA;
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Modified-site
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28-JAN-1993;
14-APR-1993;
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23-DEC-1992;
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ID AAR
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                                                                                                                                                                                                                                                                                                               This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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    used for treating or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
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Pred. No. 4.1e-10;
0; Mismatches 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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                                                                                                                                                                                                                                  New active para-thyroid hormone variants
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                                                                                                                                                                  Waelchli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waelchli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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92GB-00026415.
92GB-00026859.
92GB-00026861.
93GB-00001691.
93GB-00001692.
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92GB-00026415.
92GB-00026859.
92GB-00016861.
93GB-0001691.
93GB-0001692.
93GB-00001693.
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1 Similarity 87.1%;
27; Conservative (
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                                                                                                                                                                                                                                                   osteoporosis etc
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                                                                                                                                                                  Schneider H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [Ala1] -hPTH(1-36) -NH2
                                                                                                                                                                                                WPI; 1994-018352/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                  (SANO ) SANDOZ LTD
                                                                                                                                                                                                                                                                                                                                                                                       hypoparathyroidism
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
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Modified-site
 18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
                                                                 28-JAN-1993;
14-APR-1993;
19-APR-1993;
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18-DEC-1992;
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23-DEC-1992;
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                                                     28-JAN-1993
                                                                                                                                                                                                                                                   preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lewis I,
                                                                                                                                                                  Lewis I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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/note= "N-alpha-methyl-Ala replaces wild-type Ser residue
at position 1"
                                                                               This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone
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New active para-thyroid hormone variants - used for treating preventing osteoporosis etc.
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                                                                                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                Score 128; DB 2;
Pred. No. 4.1e-10;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-alpha-methyl[Ala1] parathyroid hormone(1-38)
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                                                                                                                                                                                                                                                                                                                                                                         31
                                                                                                                                                                                                                                                                                                                                                                                             New active para-thyroid hormone variants
                                                                                                                                                                                                                                                                                                                                                                         1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waelchli R,
                                                                      Example 260; Page 46; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 34; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR58019 standard; peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92GB-00015009.
92GB-00026415.
92GB-00026819.
92GB-0001691.
93GB-00001692.
                                                                                                                                                                                                                                                                                    80.0%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93GB-00014384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing osteoporosis etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                        PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tetherl; osteoporosis.
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0
                                                                                                                                                                                                                                                                                                                                             Parathyroid hormone functional domain conjugate peptide PG9.
                                                                                       Match 80.0%; Score 128; DB 2; Length 38; Local Similarity 87.1%; Pred. No. 4.4e-10; es 27; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .5
/label= PTH N-terminal_signaling_domain
/note= "residues 1-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15. .31
/label= PTH C-terminal binding_portion
/note= "residues 15-31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potts JT, Jueppner H;
                                                                                                                                                                    1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                       AAY96974 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 93; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5. .14
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gardella TJ, Kronenberg HM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0114577P
                                                                                                                                                                                                                                                                                                                 31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-452384/39.
N-PSDB; AAA51731.
                                                               Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200039278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-2000.
                                                                                                                                                                                                                                                                                    AAY96974;
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                            Best Loca
Matches
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CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether1 activity, increasing CAMP

CC in a mammalian cell having PTH-1 receptors, or acreening for a peptide or

CC inhalation unlike the large native PTH or PTHrP which avoids the need for

CC inhalation unlike the large native PTH or PTHrP which avoids the need for

CC regular injections to treat osteoporosis

XX

Query Match

Pest Local Similarity 87.1%; Score 127; DB 3; Length 31;

Best Local Similarity 87.1%; Preci. No. 4.8e-10;

Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSEIGLAMGGGGGLNSMERVEWLRKKLQDV 31

Db 1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31

Search completed: November 21, 2005, 16:10:11
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; Search time 23.5 Seconds
{without alignments}
126.924 Million cell updates/sec
5.1.6
Compugen Ltd.
                                                                                                                                                                                     1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
 GenCore version (c) 1993 - 2005
                                                                                          November 21, 2005, 16:05:13
                                                             sw model
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Gapop 10.0 , Gapext 0.5
                                                           protein search, using
                                                                                                                                                        US-09-475-158A-3
160
                Copyright
                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                  Scoring table:
                                                             OM protein
                                                                                                                                                                                      Sequence:
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283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

length: 0 length: 2000000000 Bed sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	parathyroid hormon	choline O-acetyltr	choline O-acetyltr	carnitine O-acetyl	probable receptor	PTS lichenan-speci	sigma 1 protein -	sigma 1 protein -	carnitine acetyltr	choline O-acetyltr	choline O-acetyltr	tldD homolog slr08	hypothetical prote			hypothetical prote	kinesin homolog KH	L-ascorbate peroxi	ಹ	moaD protein (impo	hypothetical prote	DNA-directed RNA p	mayalonate hinace						
OI 1	PTHU	PTB0	PTPG	JC4202	A05091	: I51851	A34937	B43777	A48319	A55720	T03784	: D69651	HMXRH2	: C34829	\$ \$52782	2 A39961	2 A60202							2 T10190		2 T45539	2 T45980	2 F82336	נמאמזים
Length DB	115 1	115 1	115 1	115 2	115 2	105 2	119 2	641 2	644 2	626 2	990	110 2	399 1	462 2	627 2	641 2	748 2		•	627 2				421 2		588	319	'n	
Query Match	78.1	74.4	73.1	72.5	68.8	65.6	53.1	38.8	38.8	37.5	36.9	35.6	35.0	35.0	35.0	35.0	35.0	34.4	34.4	33.8	33.1	•	32.5	32.2	31.9	31.9	31.6	31.6	21.2
Score	125	119	117	116	110	105	85	62	62	9	59	57	26	26	26	56	26	55	55	54	53	52	52	51.5	51	51		50.5	10
Result No.	-	7	m	4	ß	9	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	20

retinoblastoma bin hypothetical prote	hypothetical prote	pur operon repress	activator of purin	acetyl xylan ester	probable DNA bindi	choline O-acetyltr	choline O-acetyltr	hypothetical prote	virulence-associat	virulence associat	parathyroid hormon	_	MgPa operon hypoth	amidase (EC 3.5.1.
I58383 T00637	H83405	E95231	G98095	E72421	T03605	A36526	A24889	T45997	T09450	C64559	S10202	G72698	A64221	C42725
7	~	N	~	7	~	0	~	7	7	7	-	~	ч	~
1257	158	275	275	325	425	720	728	219	94	94	176	301	361	206
31.2	30.9	30.9	30.9	30.6	30.6	30.6	30.6	30.3	30.0	30.0	30.0	30.0	30.0	30.0
20	49.5	49.5	49.5	49	49	4	4	48.5	48	48	48	48	48	48

### ALIGNMENTS

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SULT	
3	5

parathyroid hormone precursor [validated] - human N;Alternate names: proparathyroid hormone C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004 C;Accession: A19339; S53790; A3169; S21199; A93789; A93783; A90387; A90426; A94410; I38 R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983 A;Title: Nucleotide sequence of the human parathyroid hormone gene. A;Reference number: A19339; MUID:83169834; PMID:6220408

A;Molecule type: DNA MyResidues: 1-115 «VAS.» A;Residues: 1-115 «VAS.» A;Cross-references: UNIRROT:PO1270; UNIPARC:UPI000013290A; GB:J00301; NID:g190702; PIDN: R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K. Biol. Chem. Hoppe-Seyler: 375, 921-824; 1994 A;Title: Purification of meprin from human kidney and its role in parathyroid hormone de A;Reference number: S53790; MUID:95225988; PMID:7710697

A; Accession: S53790

A,Molecule type: protein
A,Residues: 'X',33-46,65-84,105-110 <YAM>
A,Residues: 'X',33',X',35-46,65-84,105-110 <YAM>
A,Residues: 'X',33',X',35-46,65-84,105-110 <YAM>
A,Residues: 'X',33',X',35-46,65-84,105-110 <AIDPARC:UPI00001734E3
A,Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E3
A,Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurre
R,Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
A,Title: Structural analysis of human proparathyroid hormone by a new microsequencing a‡
A,Reference number: A93169; MUID:74174967; PMID:4833516

A,Molecule type: protein A,Residues: 26-37 <JAC> A,Cross-references: UNIPARC:UP100001734E4 A,Cross-references: UNIPARC:UP100001734E4 R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.1 Eur: J. Biochem: 205, 311-319, 1992

A, Title: Isolation and characterization of two biologically active O-glycosylated forms

ation. A;Reference number: S21199; MUID:92209518; PMID:1555591

A; Accession: S21199

A,Molecule type: protein A,Residues: 32-114,'N' <OLS> A,Cross-references: UNIPARC:UP10001734E5

A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation, R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H Proc., Natl. Acad. Sci. US.A. T., 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid A;Reference number: A93789; MUID:74111656; PMID:4521809

A;Molecule type: protein
A;Residues: 32-68 <NIA>
A;Residues: 32-68 <NIA>
A;Cross-references: UNIPARC:UP1000002DA05
R;Brewer Jr. H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D. Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

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A;Residues: 1-115 <WE2>
A;Gross-references: UNIPARC:UP10000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g
R;Weaver, C.A.; Gordon, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: 15975
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62
         1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
                                                                                                         RESULT 2
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A,Title: Numan parathytoid hormone; amino-acid sequence of the amino-terminal residues 1 A,Ficle: Numan parathytoid hormone; amino-acid sequence of the amino-terminal residues 1 A,Foccedue (1975) and 18783; MINI-190042; PRID 450319
A,Foccedue (1975) and 18783; MINI-19000017485
A,Focced: references (1976) and 18784; MINI-19000017485
A,Focced: references (1976) and 18784; MINI-19000017485
A,Focced: Reference number: A00387; MINI-1914871 and 1878501 burners.
A,Focced: MIPPRC, UPPRC, UPPRC, UPPRC, PRID 187501
A,Focced: A,Focced: MIPPRC, UPPRC, UPPRC, PRID 187501
A,Focced: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyfunction: factor in homeostatic control of plasma calcium and phosphate; released counter to calcitonin cyperfamily: parathyroid hormone; parathyroid hormone homology cykeywords: calcium; hormone; parathyroid gland; plasma F;1-25/Domain: pignal sequence #status predicted cSIG> F;26-31/Domain: propeptide #status experimental cPRO> F;30-64/Domain: parathyroid hormone homology cPTH> F;31-64/Domain: parathyroid hormone hatclus experimental cMAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.9
Matches 26; Conservative
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A;Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:g558915; PIDN: C;Superfamily: parathyroid hormone; parathyroid hormone homology C;Keywords: hormone P;1-31/Domain: signal sequence #status predicted <SIG>P;1-31/Domain: parathyroid hormone homology <PTH>P;30-64/Domain: parathyroid hormone homology <PTH>P;310-64/Domain: parathyroid hormone #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A05091
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-115 <HEL>
A;Cross-references: UNIPROT:P04089; UNIPARC:UPI000013290C; GB:K01268; NID:g206483; PIDN:
A;Note: the authors translated the codon GAA for residue 87 as Asp
B;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: A26806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and A,Reference number: JC4201, MUID:95369696; PMID:7642102
                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: JC4202
Krosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A;Title: Sequences of the CDNAs encoding canine parathyroid hormone-related protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Darachyroid hormone precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05091; A26806
B;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
                                                                                                                                                                                                                                                                                                 parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep_1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
   Gaps
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Pred. No. 2.9e-08;
2; Mismatches 5; Indels
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C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 115;
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A;Residues: 1-115 <SCH>
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 110; DB 2; Len
   4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
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3; Mismatches
   Mismatches
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                                                                  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
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74.2%;
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Best Local Similarity 77.44
Matches 24, Conservative
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Matches 23; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-115 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: JC4202
   24;
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      Matches
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C;Species: Sus scrofa domestica (domestic pig)
C;Accession: B26806; A90330; A90376; A01535
R;Schmelzer, H.J.; Gross, G; Widera, G.; Mayer, H.
Nuclectica Acids Res. 15, 6740, 1987
A;Title: Nuclectide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Reference number: MNYPOT:P01269; UNIPARC:UP1000013290B; GB:X05722; GB:Y00409; NID:g16
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemietry 14, 361-3635; 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial aminc
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Residues: 26-115 - CCHU>
A;Cross-references: UNIPARC:UP100001592DF
A;Residues: 26-115 - CCHU>
A;Residues: 26-115 - CCHU>
A;Residues: 26-115 - CCHU>
A;Residues: 27-115 - CCHU>
A;Residues: 28-115 - CCHU>
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Reference number: A90376; MUID:74253317; PMID:4840833
Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: 145976; MUID:83105964; PMID:6185374
A;Accession: 145976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-115 -WE3-
A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-115/Product: propeptide #status predicted <SIG>F;26-115/Product: parathyroid hormone #status experimental <PRO>F;30-64/Domain: parathyroid hormone #status experimental <MAT>F;32-115/Product: parathyroid hormone #status experimental <MAT>F;32-115/Product: parathyroid hormone #status experimental <MAT>
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A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
A,Estiques: 32-109 <8AU>
A,Cross-references: UNIPARC:UPI00001734E0
A,Cross-references: UNIPARC:UPI00001734E0
A,Cross-references: UNIPARC:UPI00001734E0
A, J. Med. 56, 759-766, 1974
A,Title: Recent studies on the chemistry of human, bowine and porcine parathyroid hormon
A,Reference number: A90030; MUID:74173303; PMID:4598526
A,Contents: annotation
C,Superfamily: parathyroid hormone; parathyroid hormone homology
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30-64/Domain: parathyroid hormone homology <PTH>
32-115/Product: parathyroid hormone #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 115;
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Best Local Similarity 80.6
Matches 25; Conservative
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Best Local Similarity
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Gaps

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Gaps

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A481916 O-acetyltransferase (EC 2.3.1.6) - rat
Cispecias: Ratura norregical (Norway zat)
Cispecias: Ratura norregicals (Norway zat)
Cispecias: A84319, A3777, A48981; A56876
A; Reterence number: A48319, MUD10-89362560; PMID:2570161
A; Reterence number: A48319
A; Reterence number: A4377
A; Reterence number: A4377
A; Reterence number: A4377
A; Reterence number: A43777
A; Reterence number: A49881; MUD:9015185; PMID:9181893
A; Title: Partial cloning of the rat choline acetyltransferase gene and in situ localizatii A; Recession: A49881; MUD:9164851; PMID:9181893
A; Title: Partial cloning of the rat choline acetyltransferase gene and in situ localizatii A; Recession: A49881
A; Rederence extracted from Worth Lackbone (NCBIN:124964, NCBIP:124965)
A; Rederence number: A49881; MUD:91240983; PMID:8479291
A; Recession: A56976
A; Residues: Preliminary
A; Reterence number: A56976
A; Reterence num
R; Ishii, K.; Oda, Y.; Ichikawa, T.; Deguchi, T.

Brain Res. Mol. Brain Res. 7 151-159 1990

A; Title: Complementary DNAs for choline acetyltransferase from spinal cords of rat and mc A; Reference number: A43777; MUID:90251122; PMID:2160042

A; Accession: B43777

A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residuces: Lef4 crSh3
A; Residuces: Lef4 crSh3
A; Rimiawa, H.; Ishii, K.; Deguchi, T.
J. Biol. Chem. 267, 20399, 1992
A; Title: Gene expression of mouse choline acetyltransferase. Alternative splicing and ide
A; Reference number: A44023; MUID:93015919; PMID:1400357
A; Accession: A44023; MUID:93015919; PMID:1400357
A; Residuces: L-219 cMIS>
A; Cross-references: UNIPARC:UPIO00016CC80; GB:D12487; NID:9220366; PIDN:BAA02056.1; PID:g:
A; Cross-reference extracted from NCBI backbone (NCBIP:115801)
C; Superfamily: carnitine O-acetyltransferase
C; Reywords: acyltransferase; coenzyme A
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.8%; Score 62, Best Local Similarity 51.9%; Pred. No. Matches 14; Conservative 2; Mismatch
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PA4937

PA4937

PA4937

PA4937

PARESOLE 68

PA
                                                                                                                      parathyroid hormone - rat (fragment)
parathyroid hormone - rat (fragment)
C(Species: Rattus norvegicus (Norway rat)
C(Species: Rattus normalizar, Rat
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C:Species: Mus musculus (house mouse)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accesion: B43777; A44023
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R;Xu, Y:; Zhu, Q:; Lamb, C.
submitted to the EMBL Data Library, June 1995
A;Description: Molecular cloning and characterization of a rice gene encoding leucine-rl,
A;Reference number: Z15083
A;Accession: T03784
A;Accession: T03784
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reciule type: DNA
A;Residues: 1-990 <XUY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: 1rk2
A;Introns: 870/1
C;Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat ho
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C;Date: 05-Dec-1997 #Sequence_revision 05-Dec-1997 #text_change 31-Dec-2004
C;Accession: D69651; S57761
R;Kunst, F; Ogsawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Bhrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Natute 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, K.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadain, Y.; Sako, A.; Sacho, T., Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Yamano, C. M.; Yamano, K.; Yoshida, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Atters genome sequence of the Cram-Positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.cross-references: UNIPROT:P46319; UNIPARC:UPI000060C4F; GB:Z99123; GB:AL009126; NID:g
A.Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000060C4F; EMBL:249992; NID:9895746; PIDN:CAA90287.1; Pİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: UNIPROT:040699; UNIPARC:UP100000A9030; EMBL:X89226; NID:g1263159; Pt
A.Experimental source: cv. IR36, leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: phosphotransferase system, lactose/cellobiose-specific component IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: D69651
Status: preliminary; nucleic acid sequence not shown; translation not shown; Ambecule type: DNA
                                                                        C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTS lichenan-specific enzyme IIA component licA - Bacillus subtilis N;Alternate names: probable cellobiose phosphotransferase enzyme III C;Species: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB;
Pred. No. 8.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riglaser, P.; Lubochinsky, B.; Danchin, A. submitted to the EMBL Data Library, July 1995 A; Description: Bacillus subtilis cel operon. A; Reference number: 857758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 MRGGGGGAGSQLRLRWDSKKM 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 MHGGGGGLNSMERVEWLRKKL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.4%;
Matches 11; Conservative
                                    receptor protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                C; Accession: T03784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S57761
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A;Nap position: 9434.1-9434.1
A;Note: at least one intron occurs before the initiator of the peroxisomal form
c;Superfamily: carnitine O-acetyltransferase precursor, mitochondrial splice form #staff:1-28/Pomain: transit peptide (mitochondrian) #status predicted cTNP>
F;1-626/Product: carnitine O-acetyltransferase precursor, mitochondrial splice form #staff:22-626/Product: carnitine O-acetyltransferase precursor, peroxisomal splice form #statff:22-29/Domain: propeptide #link MATP #status predicted cNPO>
F;29-626/Product: carnitine O-acetyltransferase, mitochondrial #status predicted cMATM>
F;30-626/Product: carnitine O-acetyltransferase, peroxisomal #status predicted cMATM>
F;30-626/Product: carnitine O-acetyltransferase, peroxisomal #status predicted cMATM>
F;50-626/Product: carnitine O-acetyltransferase, peroxisomal #status predicted cMATM>
F;624-626/Region: peroxisome/glyoxysome location signal #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
A55720
Carnitine O-acetyltransferase (EC 2.3.1.7) precursor, mitochondrial - human
NyAlternate names: catl protein
NyContains: carnitine O-acetyltransferase, peroxisomal
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A55720; S50030; S50029
R;Corti, O.; Finocchiaro, G.; Rossi, E.; Zuffardi, O.; DiDonato, S.
Genomics 23, 94-99, 1994
A;Title: Molecular cloning of CDNAs encoding human carnitine acetyltransferase and mappi
A;Reference number: A55720; MUID:95130117; PMID:7829107
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Biochem. J. 303, 37-41, 1994
A;Title: Divergent sequences in the S' region of cDNA suggest alternative splicing as A;Reference number: $50029; MUID:95031982; PMID:7945262
                                                                                                                                                                                                                                                                                                        1;
                                A, Experimental source: spinal cord
A, Experimental source: spinal cord
A, Note: sequence extracted from NCBI backbone (NCBIN:130081, NCBIP:130082)
C, Superfamily: carnitine O-acetyltransferase
C, Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                        Gaps
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A;Molecule type: mRN
A;Residues: 22-626 «CO2>
A;Cross-references: UNIPROT:P43155; UNIPARC:UP1000002A53F; EMBL:X78706
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2 < COR
A;Cross-references: UNIPARC:UPI000017535F; EMBL:X79825
A;Experimental source: clone SM-1200
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A,Experimental source: clone SM-1400
                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                Query Match 38.8%; Score 62; DB Best Local Similarity 51.9%; Pred. No. 2.3; Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 LÓLLHGGGCSLNGANR--WYDKSLÓFV 321
                                                                                                                                                                                                                                                                                                                                                                                     5 IQLMHGGGGGLNSMERVEWLRKKLQDV 31
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A; Cross-references: UNIPARC: UPI000017535D
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A; Residues: 22-52 < CO3 >
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A,Gene: GDB:CRAT; CAT1
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ò 셤 DB 2; Length 110;

35.6%; Score 57;

Query Match

1;

Gaps

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C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S22782
R;Brunner: S.; Kramar, K.; Hofbauer, R.
submitted to the EMBL Data Library, March 1995
A;Pescription: A novel cell cycle regulated carnitine acetyltransferase in S3T3 cells.
A;Reference number: S52782
A;Accession: S25782
A;Accession: S25782
A;Accession: S2782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.0%; Score 56; DB 2; Length 627; Best Local Similarity 50.0%; Pred. No. 14; Matches 12; Conservative 2; Mismatches 8; Indels
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Job time : 24.5 secs
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C34829

signal protein - recovirus type 2 (strain Jones)

NyAlternate names: hemagglutinin; minor outer capsid protein
C;Species: recovirus type 2

C;Species: recovirus type 2

A;Note: nose Homo sapiens (man)
C;Date: nose Homo sapiens (man)
C;Date: nose Homo sapiens
C;Date: nose Homo sapiens
C;Accession: C34829

A;Nibert, M.L.; Dermody, T.S.; Fields, B.N.
J. Virol. 64, 2976-2288, 1990
A;Title: Structure of the recovirus cell-attachment protein: a model for the domain organ
A;Reference number: A34829; MUID:90244415; PMID:2335823
A;Reference number: A34829; MUID:90244415; PMID:2335823
A;Redius: preliminary
A;Rocession: C34829
A;Redius: 1-462 < NIBA
A;Redius: segment S1
C;Superfamily: recovirus sigma 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATALE DETOCETION - REOVINES type 2

Nighternate names: hemagalutinin
C;Species: reovirus type 2

A;Note: host Homo sapiens (man)
C;Species: reovirus type 2

A;Note: host Homo sapiens (man)
C;Species: reovirus type 2

A;Note: host Homo sapiens (man)
C;Species: reovirus type 2

A;Note: host Homo sapiens (man)
C;Accession: Ad4123

R;Cashdollar, L.W., Chmello, R.A., 82, 24-28, 1985

R;Cashdollar, L.W., Chmello, R.A., 82, 24-28, 1985
A;Title: Sequences of the S1 genes of the three serotypes of reovirus.
A;Reference number: A94035; MUID:85113159; PMID:3855545
A;Accession: Ad4123
A;Accession: Ad4123
A;Accession: Ad4123
A;Residues: 1-399 cCAS>
A;Cross-references: UNIPROT:P04507; UNIPARC:UPI0000163913; GB:MI0261; NID:9808813; PIDN:
C;Genetics: S1; sigma 1
C;Superfeanily: reovirus sigma 1 protein
C;Keywords: glycoprotein; hemagglutinin
C;Keywords: glycoprotein; hemagglutinin
C;Keywords: glycoprotein; hemagglutinin
C;Keywords: 297/Binding site: carbohydrate (Asn) (covalent) #status predicted
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35.0%; Score 56; DB 1; Length 399;
Best Local Similarity 35.7%; Pred. No. 8.8;
Matches 10; Conservative 8; Mismatches 10; Indels
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35.0%; Score 56; DB 2; Length 462;
Best Local Similarity 35.7%; Pred. No. 10;
Matches 10; Conservative 8; Mismatches 10; Indels
                                                                                        6; Indels
                                                                                                                                                                                      7 LMHGGGGGLNSMERV-----EWLRKKLQD 30
                                                                                                                                                                                                                                                 Best Local Similarity 40.6%; Fred. No. 1.7; Matches 13; Conservative 5; Mismatches
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RESULT 15 8527182 Carnitine acetyltransferase - mouse C;Species: Mus musculus (house mouse)

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CB30 HYDMC
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## ALIGNMENTS

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MUCLEOTIDE 3169834; PubMed=6220408;
Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N., Vasicek T.J., Rich A., Kronenberg H.M.;
Potts J.T. Jr., Rich A., Kronenberg H.M.;
"Nucleotide sequence of the human parathyroid hormone gene.";
Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
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MEDLINE=74174967; PubMed-48131516;
Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
"Structural analysis of human proparathyroid hormone by a new
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MEDLINE-4111656; Pubmed-4521809;
Miall H.D., Sauer T., Jacobs J.W., Keutmann H.T., Segre G.V.,
O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
                                                   21-JUL-1986 (Rel. 01, Created)
13-MG-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 08, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone)
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;

"Signal peptide prediction based on analysis of experimentally verified cleavage sites:";

Protein Sci. 13:2819-2824(2004).
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MEDLINE-79082855; PubMed-728431;
Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981)
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                  115 AA
                  PRT;
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NUCLEOTIDE SEQUENCE.
MEDLINE=82150870; PubMed=6950381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microsequencing approach.";
Nature 249:155-157(1974).
                    STANDARD;
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                    PTHY HUMAN
                                                                                                                               Name=PTH;
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                                      P01270;
PTHY HUMAN
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SMART; SM00087; PTH; 1
PROSITE; PS00335; PARA
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   TRUCTURE BY NMR OF 32-65.

MEDLINE=31299748; PubMed=2069952;

MEDLINE=31299748; PubMed=2069952;

MINVESTIGATION OF the MEDLIAN STRUCTURE OF The human parathyroid investigation of the solution structure of the human parathyroid hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and molecular dynamics calculations."; pectroscopy, distance geometry, and biochemistry 30:6936-6942(1991).
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MEDLINE-ZOOGG19, PUBMed=10623601, DOI=10.1006/bbrc.1999.1958,
MEDLINE-ZOOGG19, PUBMed=10623601, FORESmann W.-G., Rosch P.;
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Blochem. Blochys. Res. Commun. 267:213-220(1000).
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MEDINE-5146516; PubMed=1125201;
MEDINE-5146516; PubMed=1125201;
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MEDLINE=75059220; bubMed=4474131;
Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,
Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
"Solid-phase synthesis of the biologically active N-terminal 1-34
peptide of human parathyroid hormone ";
Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
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STRUCTURE BY NWR OF 32-68.
STRUCTURE BY NWR OF 32-68.
MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
Roesch P.;
                                                                                                                        Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N., O'Riordan J.L.H., Potts J.T. Jr.; (In) Talandge R.V., Owen M., Parsons J.A. (eds.); Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).
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Barden J.A., Cuthbertson R.M.;
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MSDLINE-91009B11; PubMed=2212001;
Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
Kronenberg H.M.;
Kronenber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIS OF 32-65.

Madilane 3227467; PubMed=4721748;

Andreata R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
Riniker B., Rittel W., Sieber P.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 32-65.
MEDLINE=93345518; PubMed=8344299;
                                                                                                            PROTEIN SEQUENCE OF 75-100.
Keutmann H.T., Niall H.D.,
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PubMed=10523031;
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An incurrent hepotracial T. Churenigaes S. Wgongsarthyroid
T. A novel mattion of the signal peptide of the preproparthyroid
The formon gene associated with autoeomal recessive familial isolated
Phypoparathyroidism.'

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Matches

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;
Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.1%; Score 125; DB 2; Length 115; 83.9%; Pred. No. 1.3e-08; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARATHYROID; 1.
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Mammalia, Eutheria, Laurasiatheria, Perissodactyla;
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Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC096143; AAH96143.1; -; mRNA.
EMBL; BC096144; AAH96144.1; -; mRNA.
EMBL; BC096145; AAH96145.1; -; mRNA.
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InterPro; IPR003625; Pthyrhorm_sub.
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PIRSF; PIRSF001832; PTH; 1.
ProDom; PD010687; Pthyrhorm sub; 1.
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Parathyroid hormone (Fragment).
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NIH MGC Project;
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sapiens (Human)
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SEQUENCE 115 AA;
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Malalavijitnond S., Takenaka O.;
"Nucleotide sequences of parathyroid gene in five species of macaque
of Thailand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
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NGBI TaxID=9541.
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                   Indels
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26 31 By similarity.
32 115 Parachyroid hormone.
115 AA, 12890 MW, 8C2500EP24BE5597 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyrid hormone, preproprotein.
                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MRY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.1%; Score 125; DB 1; Best Local Similarity 83.9%; Pred. No. 1.3e-08; Matches 26; Conservative 1; Mismatches 4.
    Pred. No. 1.3e-08;
1; Mismatches 4
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                                                                     1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                               115 AA
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HSSP; P01270; 1ET1.
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InterPro; IPR003625; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
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                                                                                                                                                               PRT;
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   83.9%;
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Q4VB48;
                       26; Conservative
                                                                                                                                                               STANDARD;
      Similarity
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Gaps

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Euteleostomi; Equidae; Equus.

RESULT 3

ઠે 셤 04VB48 1D 04 AC 04 DT 13 DT 13 DE PA

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Gene 28:319-329(1984).
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MUCLEOTIDE SEQUENCE.

Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A., Potts J.T. Jr., Rich A.;

Fotts J.T. Jr., Rich A.;

Folloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone.";

Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE.
NUCLECTION SEQUENCE.
NUCLECTION SEQUENCE.
NEDLINE=82033785; PubMed=6170060;
NEAVOR C.A., Gordon D.F., Kemper B.;
"Introduction by molecular cloning of artifactual inverted sequences
"Introduction by molecular cloning of artifactual inverted sequences
at the 5' terminus of the sense strand of bovine parathyroid hormone
at the 5' terminus of the sense strand of bovine parathyroid hormone
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WICLEOTIDE SEQUENCE.

MEDLINE=83105564; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8; Meaver C.A., Gordon D.F., Kemper B.; Weaver C.A., Gordon D.F., Kemper B.; "Nucleotide sequence of bovine parathyroid hormone messenger RNA."; Mol. Cell. Endocrinol. 28:411-424(1982).
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MEDLINE=64262463; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5; Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.; Isolation and complete nucleotide sequence of the gene for bovine parathyroid hormone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1229-1249(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 AA; 9805 MW; 253184EA681A2022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 2;
Pred. No. 3.2e-08;
2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SVSEIQLMHNLGKHLNSVERVEWLRKKLQDV 33
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SEQUENCE
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PIHY BOOIN
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DY 21-JUL-
DT 21-JUL-

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Matches
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WEDLINE-701266; PubMed-512270;
AM HELLING J. W. A. Nall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr., MEDLINE-701266; PubMed-512270;
AM HELLION J.W., Nall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr., A. COHN D.V.;
COHN D.V., A. Mall H.D., A. Wall H.D., Sauer R., Hogan W.L., Dawson B.F., A. MIDSHER-7107612; PubMed-521011;
AM MAILH H.D., Keutmann H.T., Sauer R., Hogan W.L., Dawson B.F., A. MIDSHER-7107612; PubMed-521011;
AM MIDSHER-7107612; PubMed-5275134;
AM MIDSHER-7107612; PubMed-527514;
AM MIDSHER-7107612; PubMed-527516;
AM MIDSHER-7107612; PubMed-527516;
AM MIDSHER-7107612; PubMed-527516;
AM MIDSHER-7107612; PubMed-527516;
AM MIDSHER-7107614;
AM MIDSHER-7107612;
AM MIDSHER-7107614;
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PROPEP
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ID Q8
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=74253317; PubMed=4840833; Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H., Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H., Potts J.T., Jr.; Plant amino acid sequence of porcine parathyroid hormone."; Biochemistry 13:1994-1999(1974).

-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

-!- SIBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
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MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
"Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metāzoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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74.4%; Score 119; DB 1; Length 115; 80.6%; Pred. No. 8e-08; 1; Mismatches 5; Indels
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9FE9BCDE614BAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                     115 AA
                                                                                                                                    1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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SIGNAL 1 25
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InterPro; IPR001455; Pthyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub; 1.
Pfam; PP01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
SWART; SM00087; Prhyrhorm_sub; 1.
PROSITE; PS00335; PARATHYROID; 1.
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PIR; B26806; PTPG.
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Query Match
Best Local Similarity 80.6'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig)
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SEQUENCE
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PTHY PIG
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                            Gaps
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MEDLINE=9536966; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone.";

Gene 160:241-243(1995).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Query Match 73.1%; Score 117; DB 1; Length 115; Best Local Similarity 77.4%; Pred. No. 1.5e-07; Matches 24; Conservative 3; Mismatches 4; Indels
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By similarity.
Parathyroid hormone.
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Ensembl; ENSCAFG0000008177; Canis familiaris.
EnterPro; 1PR001415; Parathyrd_hrm.
InterPro; 1PR001415; Parathyrd_hrm.
InterPro; 1PR003625; Pthyrhorm_sub; 1.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
PIRSF; PIRSF001832; PTH; 1.
Probom; PD010687; PTH; 1.
SMART; SM00087; PTH; 1.
                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
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                                                                                                                                        SUSEIQLMHNLGKHLSSLERVEWLRKKLQDV
                                                                                                             1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
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PIR; JC4202; JC4202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00335; PARATHYROID; 1.
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                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
31
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
01-OCT-1996
10-MAY-2005
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                                                                                                                                                                                                                                                                                                 CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PTH;
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Endoctrinology 136:5600-5607(1995).

- Incontaction and preventing their renal excretion.

- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

- STRUBGELLULAR LOCATION: Secreted.

- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.

- SIMILARITY: Belongs to the parathyroid hormone family.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation the European Bioinformatics in no way modified and this statement is not
                               Schmelzer H.J., Gross G., Mayer H.; "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTHY PELCA STANDARD; PRT; 115 AA.
09GL67.
10-MAY-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid (Armone precursor (Parathyrin) (PTH).
Name-PTH;
Pelis silvestris catus (Cat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 32-115.
STRAAL-Spraque-Dawley; TISSUE-Brain, Liver, and Parathyroid;
MEDLINE-96079910; Pubmed-758814; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ibonucleic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.8%; Score 110; DB 1; Length 115; Best Local Similarity 74.2%; Pred. No. 1.3e-06; Matches 23; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
31 Parathyroid hormone.
18 C -> Y (in Ref. 3).
23 A -> T (in Ref. 3).
33 V -> I (in Ref. 3).
62 V -> G (in Ref. 3).
62 V -> G (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K01268; AAA41979.1; -; Genomic_DNA.
EMBL; X05721; CAA29192.1; -; mRNA.
EMBL; M84875; AAA77156.1; -; mRNA.
EMBL; S80127; -; NOT_ANNOTATED_CDS; mRNA.
FRIS, 280127; -; NOT_ANNOTATED_CDS; mRNA.
FIR; A05091; A05091.
HSSP; P01270; IZWB.
Ensembl; BNSNCOGOOO014318; Rattus norvegicus.
RGD; 3440; Pth.
Inte-Pro; IPR003626; PTH_related.
Inte-Pro; IPR003626; PTH_related.
Inte-Pro; IPR003626; PTH_related.
PANTHER; PTHR10541; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub.
PRODOM; PD010609; PTH_related; 1.
ProDom; PD010609; PTH; Lalated; 1.
SWART; SWO0087; PTH; Lalated; 1.
SIGNAL STORM; PD010609; PTH; Lalated; 1.
SWART; SWO0087; PTH; Lalated; 1.
SWART; SWO0087; PTH; Lalated; 1.
SIGNAL STORM; PD010609; PTH; Lalated; 1.
SWART; SWO0087; PTH; Lalated; 1.
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                                                                               hormone.";
Adv. Gene Technol. 21:228-229(1984).
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32
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62
115 AA;
   TISSUE=Parathyroid;
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SEQUENCE
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PTHY FELCA
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080WZ2;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Name-PTH-11-84);
Name-PTH-11-84);
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
NCBL_TaxID=10116;
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Muranalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
NUIO LaxID=10116;
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Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.P.;
"Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.", Brol. chem. 259:3320-3329(1984).
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 68.8%; Score 110; DB 2; Length 10
1 Similarity 74.2%; Pred. No. 1.1e-06;
23; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00335; PARATHYROID; 1.
SEQUENCE 105 AA; 11684 MW; 18EE71B3F1CF5F70 CRC64;
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PTHY RAT

AC P04089; O63473;
DT O1-NOV-1986 (Rel. 03, Created)
DT O1-NOV-1986 (Rel. 03, Last sequence update)
DT O1-NOV-1986 (Rel. 04), Last sequence update)
DT O1-NOV-1986 (Rel. 04), Last sequence update)
DT O1-NOV-1986 (Rel. 07), Last sequence update)
DT O1-NOV-1986 (Rel. 07), Last sequence update)
DT ONMERSTORE (Rel. 07), Last sequence update)
DE Parathyproid hormone precursor (Parathyrin) (PTH).
GN Name=Pth;
GN Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia Nucleoria Marinae; Marinae; Rattus.

NUCLEOTIDE SEQUENCE.
RX MBDLINE=84135846; PubMed=6321505;
RX MBDLINE=84135846; PubMed=6321505;
RY Gene encoding parathyroid hormone. Nucleoride sequence of rat prepropanty of the mone.

RT Gene and deduced amino acid sequence of rat prepropanty of the mone.

RT Gene and deduced amino acid sequence of rat prepropanty of the moleoride sequence of all1-length cDNA clone encompagarathyroid hormone from pig and rat.;

RI Nucleoride sequence of all1-length cDNA clone encompagarathyroid hormone from pig and rat.;

RN NUCLEOTIDE SEQUENCE OF 10-115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endocrinology 136:5600-5607(1995).
EMBL, S80127, AAP32220.1; -; mRNA.
HSSP, P01270; 1ZWB.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
INCEPPO; IPR001415; Parathyrd hrm.
INCEPPO; IPR003625; Pthyrhorm sub.
PANTHER; PTHRIO1941; Pthyrhorm = ub; 1.
PIRSF: PTRSFC01832; PTH; 1.
PLODOM; P010687; Pthyrhorm = ub; 1.
PRODOM; P010687; Pthyrhorm = ub; 1.
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                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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Gaps

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MEDLINE=89219100; PubMed=2710135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA; 12825 MW;
                                                                                                                                                                                                                                                                                                                     sednences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken)
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NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Thyroid;
                                                                                                                                                                                                                                                                                                                 and mouse cDNA
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P15743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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PTHY_CHICK
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                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                        Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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                                                                                                                                                                                                                           SUBCELLULÂR LOCATIÓN: Secreted (By similarity). SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 68.1%; Score 109; DB 1; Length 11 Local Similarity 71.0%; Pred. No. 1.7e-06; nes 22; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
By similarity.
Parathyroid hormone.
; 80CD557CC6AlA47E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 10, Last sequence update) (TrEMBLrel. 31, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 SVSEIQFWHNLGKHLSSVERVEWLRRKLQDV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Pfan; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; P0010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF309967; AAG30545.1; -; mRNA.
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31 BY
115 PA
12921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, La Parathyroid hormone precursor.
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Q9Z0L6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
32 1
115 AA;
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                     Felinae, Felis.
NCBI_TaxID=9685;
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    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Pth;
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                                                                                                                                                                                                                                                                                                                                                                                             removed.
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caarunci T.L., Scheetz T.E., Bromatein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A. Raha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.B., Mullahy S.J., Nrilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Palton E., Ketteman M., Madan A., Caxina A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A. Rodriguez A.C., Grimwood J., Schwutz J., Misers R.M., Schnerch A., Schein J.E., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parathyroid hormone.
DA43FABBCB4E2FD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; PO1270; JAM. PO1270; MARCHARD, PO1270; MARCHARD, PO1270; LZWB.

Ensembl; ENSWUSG0000059077; Mus musculus.

MG1; MG1:97799; Pt.

G0; G0:0005615; C:extracellular space; IDA.

G0; G0:0005179; F:hormone activity; IDA.

G0; G0:0005179; F:hormone activity; IDA.

InterPro; IPR001415; Parathyrd.hrm.

InterPro; IPR001415; Parathyrd.hrm.

PANTHER; PTHR10541; Pthyrhorm_sub; 1.

Pfam; PF01279; Parathyroid; 1.

ProDom; PD010687; PTH; 1.

ProDom; PD010687; Pthyrhorm_sub; 1.
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67.5%; Score 108; DB 2;
Best Local Similarity 71.0%; Pred. No. 2.3e-06;
Matches 22; Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (PTH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF066075; AAC99656.1; -; Genomic_DNA.
EMBL; BC099456; AAH99456.1; -; mRNA.
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16 NSMERVEWLRKKLQD 30
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                                                                                                                                Query Match
Best Local Similarity 46...
Best 10cal 814; Conservative
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14; Conservative
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                            PTH;
                                                                                                                      91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "coincidence"
                                                                                                            SMART; SM00087;
SEQUENCE 91 AJ
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                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PubMed=14684608; DOI=10.1210/en.2003-0964;

Geneure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,

Geneure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,

Bastege M., Rubin D.A., Juppner H.;

"Identification and characterization of two parathyroid hormone-like

"Identification and characterization of two parathyroid sommone of the molecules in zebrafish.";

Endocrinology 145:1634-1639(2004).

Endocrinology 145:1634-1139(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 53.1%; Score 85; DB 1; Length 119
Local Similarity 54.8%; Pred. No. 0.0027;
Les 17; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL 1 25
PROPEP 26 31
PROPEP 36 119
PART 119 PARATHYROIG HORMONE.
SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 SVSEMQL/MINIGEHRHTVERQDWLQMKLQDV 62
                                                                                                                                                                                                                                           HSSP, PO1270; IFVY.
Ensembl; ENSCALGO000005358; Gallus gallus.
InterPro: IPR001415; Parathyrd_hrm.
InterPro: IPR003636; PTH related.
InterPro: IPR003625; Pthyrhorm_sub.
Pfam: PF01279; Parathyrorm_sub, IPR0878; PRIRIOS41; Pthyrhorm_sub, IPR0878; PRIRIOS41; Pthyrhorm_sub, IPR0879; Parathyroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                 ProDom; PD013225; PTH_related; 1. ProDom; PD010687; Pthyrhorm_sub; 1. SRART; SM0087; PTH; 1. PROSITE; PS00335; PARATHYROID; 1. Hormone; Signal.
                                                                                                                                                                                                             EMBL; M31604; AAA49093.1; -; mRNA.
EMBL; M36522; AAB02866.1; -; mRNA.
PIR; A34937; A34937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Parathyroid hormone type-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEW9J4 FUGRU PRELIMINARY;
QEW9J4;
 [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                         removed
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Matches
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-!-SIMILARITY: Belongs to the parathyroid hormone family.
-!-SAUTION: 14 of the 15 residues are identical to an internal region of human parathyroid hormone. That seems quite an incredible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE, FUNCTION, INDUCTION, AND MASS SPECTROMETRY.
TISSUB=Leaf;
MEDINE=21671918; PubMed=1181226; DOI=10.1006/prep.2001.1551;
Mang Q., Gong Z.-Z.;
"Purification and characterization of an ethylene-induced antifungal protein from leaves of Guilder rose (Hydrangea macrophylla).";
Protein Expr. Purif. 24:76-82(2002).
-!-FUNCTION: Has antifungal activity against A.alternate,
A.cucumerina, A.niger. C.gossypii, F.oxysporum, F.oxysporum subspmelonis, F.moniliforme, T.cucumeris, and V.dahliae. Has no filtinase or agglutination activities.
-!-INDUCTION: By ethylene.
-!- MASS SPECTROMETRY: WW=30010; METHOD=Electrospray; RANGE=1-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2005 (Rel. 48, Last annotation update)
Chitin-binding protein HM30 (Fragment).

Hydrangea macrophylla (Bigleaf hydrangea).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, appermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; Cornales; Hydrangeaceae, Hydrangea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.5%; Score 68; DB 2; Length 91;
46.7%; Pred. No. 0.38;
ive 6; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    10647 MW; 75BBA25CEA64BF68 CRC64;
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93.3%; Pred. No. 0.15;
iive 0; Mismatches 1
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000519; F:hormone activity; IEA.
GO; GO:0007595; P:lactation; IEA.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrborm_sub.
InterPro; IPR003625; Pthyrborm_sub.
InterPro; IPR003626; PTH related.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
ProDom; PD0110687; Pthyrhorm sub; 1.
ProDom; PD0110687; Pthyrhorm sub; 1.
ProDom; PD011055; PTH related; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (Rel. 45, Created)
15-OCT-2004 (Rel. 45, Last sequence update)
15-OCT-2004 (Rel. 48, Last annotation update)
15-28F-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 ISEVQLMHNVREHKQVGERQDWLQEKLKDV 60
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WE STANDARY S. PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0;

RA POWER D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,

RA Elgar G., Clark M.S.;

RT "Genomic structure and expression of parathyroid hormone-related

RT Genomic structure and expression of parathyroid hormone-related

RT Genomic Secondary Fugu rubripes.";

RE Gene 250:67-76(2000).

RE MBL; AJ249391; CAB94712.1; -; Genomic_DNA.

DR EMBL; AJ249391; CAB94712.1; -; Genomic_DNA.

DR ENSEMPL; SINFRUGO0000131728; Fugu rubripes.

GO; GO:0005795; F: hormone activity; IEA.

DR GO; GO:0005795; P: hormone activity; IEA.

DR GO; GO:0005795; P: hormone activity; IEA.

DR GO; GO:0005795; P: harathyrd hrm.

DR HORPERO; IPR001415; Parathyrold; 1.

REPEDOM: PD013225; PTH_related.

DR ProDom: PD013225; PTH_related; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neoperrygii; Teleostei; Euteleostei; Neoteleostei;
Acathomorpha; Acanthopterrygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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45.2%; Pred. No. 1.7;
tive 3; Mismatches 14; Indels
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163 Aa; 18698 MW; 3AC5F2C764732278 CRC64;
                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone-related protein precursor.
                                                                                         163 AA.
                                                                                         PRT;
                                                                                Q918E9 FUGRU PRELIMINARY;
Q918E9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 45.2
nes 14; Conservative
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Matches
RESULT 15
0918B2 FUG
0918B2 AC
0918B2
DT 01-0C
DT 01-0C
DT 01-1C
DE Parat
GN Nume=
OC Bukar
OC Actin
OC Actin
OC Actin
CC Actin
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Search completed: November 21, 2005, 16:15:11 Job time : 148.5 secs

SVSHAQLMHDKGRSLQEFRRRMWLHKLLEEV 68 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

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64

Sequence Sequence Sequence

Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 7,

Sequence Sequence Sequence

sequence 1, Sequence 2, Sequence 1, A Sequence 13, A Sequence 13, A Sequence 1, Ap Sequence 2, Ap Sequence 5, Apr

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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RESULT 1
US-08-142-551B-46

j Sequence 46, Application US/08142551B

j Patent No. 5814603

j Patent No. 5814603

j GENERAL INFORMATION:
   APPLICANT: Oldenburg, Kevin R.
   APPLICANT: Selick, Harold E.
   TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME CORRESPONDENCE ADDRESS:
   ADDRESSEE: Burns, Doane, Swecker & Mathis CITY: Alexandria
   STREET: 699 Prince Street
   CITY: Alexandria
   STRATE: Virginia
   COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 103
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopgatible
COMPUTER: 18M PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
FILING DATE: 14-JUN-1993
RILOR APPLICATION DATA:
APPLICATION NUMBER: US 07/098,219
FILING DATE: 12-JUN-1992
RILOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/0965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAMME: SWISS GERES GERES 1000001
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 0000324-010
US-09-447-800-9
US-07-765-373-1
US-08-03-09-1
US-08-262-495C-1
US-08-443-863-1
US-08-448-105-7
US-08-448-105-7
US-08-449-317A-1
US-08-449-317A-1
US-08-449-317A-1
US-08-449-317A-1
US-08-449-47-12
US-08-449-47-1
US-08-411-726-2
US-08-411-726-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEPAX: (415) 854-275
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 35 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: protein
       14, Appl
32, Appl
2, Appli
1, Appli
6, Appli
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Sequence 17, Appl
Sequence 18, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           November 21, 2005, 16:05:03 ; Search time 33 Seconds (without alignments) 77.665 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 162,
Sequence 163,
Sequence 52, A
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*

'GGT2 6/ptodata1/liaa/5_COMB.pep:*
'GGT2 6/ptodata1/liaa/6_COMB.pep:*
'GGT2 6/ptodata1/liaa/H_COMB.pep:*
'GGT2 6/ptodata1/liaa/H_COMB.pep:*
'GGT2 6/ptodata1/liaa/RECOMB.pep:*
'GGT2 6/ptodata1/liaa/RE
                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-447-800-5
US-09-044-516A-12
US-09-843-221A-17
US-09-843-221A-17
US-09-843-221A-162
US-09-843-221A-163
US-08-142-551B-56
US-08-142-551B-56
US-08-142-551B-56
US-08-14-551B-56
US-08-16-47C-1
US-08-904-760B-1
                                                                                                                                                                                                                                       1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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US-09-623-548A-271
US-09-657-276-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-09-536-785A-14
S-09-536-785A-32
S-09-843-221A-27
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                  US-09-475-158A-3
160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing:
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Result

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; FEATURE:
; NAMEKEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                          ò
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                          /note= "Where "Xaa" is selected from the group consisting of Hol, Ho, a homoserine amide, or the sequence of amino acids comprising residues 35-84 of PTH."
                                                                                                                                                                                                                                                                                                                                                                                                              US-09447-800-6
US-09-447-800-6
US-09-447-800-6
Sequence 6, Application US/09447800
Sequence 6, Application US/09447800
Sequence 70. 6537965
SEQUENCE 100-6537965
SEQUENCE 100-6537965
SEQUENCE 100-6537965
SETILE REPERENCE: 0609-4630001
CURRENT FILLY APPLICANTON: ANNO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENITION: ANNO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENITION: ANNO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENITION: ANNO-TERMINAL WORDER: US/09/447,800
CURRENT FILLYG DATE: 1999-11-23
SARLIER APPLICATION NUMBER: 66/110,152
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOS-19-147-800-5

Sequence 5, Application US/09447800

PRETENT NO. 6537965

GENERAL INFORMATION:
APPLICANT: BRINGHURST F. RICHARD
APPLICANT: TRANSU, HISASHI
APPLICANT: TATLE OF INVENTION: ANALOGS
FILE REPERBYCE: 0609-463001

CURRENT PAPLICATION NUMBER: US/09/447,800

FILE REPERBYCE: 1999-11-23

GENERAL PELING DATE: 1999-11-25

SAFLIER PILING DATE: 1999-11-25

SAFLIER PILING DATE: 1998-11-25

SOFTWARE: PARENT NET: 1998-11-25

SOFTWARE: PARENT NET: 1998-11-25

SEQ ID NO 5

LENGHH: 34

TYPE: PRT

CREANISM: Homo sapiens
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                             Length 35;
                                                                                                                                                                             Query Match 80.6%; Score 129; DB 1; Length 35
Best Local Similarity 80.6%; Pred. No. 5.8e-10;
Matches 25; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.0%; Score 128; DB 2; Best Local Similarity 87.1%; Pred. No. 7.3e-10; Matches 27; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
|||||||||||||||||||||||||||
1 AVSEIQLMHNLGKHINSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Desamino Ala
US-09-447-800-6
; LOCATION: 35; OTHER INPORMATION: /
; OTHER INFORMATION: 6; OTHER INFORMATION: 6; OTHER INFORMATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-447-800-5
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Sequence 162, Application US/09843221A

Sequence 162, Application US/09843221A

Sequence 162, Application US/09843221A

Sequence 162, Application US/09843221A

GENERAL INFORMATION:

APPLICANT: KOSTENUIK:

APPLICANT: LUJ, CHUNA-FA

APPLICANT: LUJ, CHUNA-FA

APPLICANT: LUJ, CHUNA-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HITLE OF INVENTION: WORDER: US/09/843,221A

CURRENT APPLICATION NUMBER: US/09-26

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-26

PRIOR PRILING DATE: 2000-04-26

PRIOR PRILING DATE: 2000-04-26

PRIOR PRILING DATE: 2000-04-26

PRIOR DATE: 2000-04-26

PRIOR DATE: 2000-04-26

PRIOR DATE: 2000-04-27

**MIMBER: 60/200,053
   ; LOCATION: (34); OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus US-09-843-221A-162
  ö
  Gaps
  ö
  Length 34;
  Indels
  Query Match
79.4%; Score 127; DB 2;
Best Local Similarity 83.9%; Pred. No. 1e-09;
Matches 26; Conservative 1; Mismatches 4
  OTHER INFORMATION: Preferred embodiments - PTH
  1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
   SVSEIQLMHNRGKHLNSMERVEWLRKKLODV 31
  TYPE: PRT
ORGANISM: Artificial Sequence
   ORGANISM: Artificial Sequence
  NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.1
  SEQ ID NO 162
   TYPE: PRT
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   셤
                  ઠે
   US-09-843-221A-18

US-09-843-221A-18

Sequence 18, Application US/09843221A

Patent No. 6756480

GENERAL INFORMATION:
APPLICANT: KOSTENUIX, PAUL
APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE APPLICANTION NUMBER: US/09/843,221A

CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: Patentin version 3.1

SEQ ID NO 18

LEMOTH: 34

LEMOTH: 34
  GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CULAN-FR.
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR PILLING DATE: 2001-02-06
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PALENTIN VETSION 3.1
LENGTH: 34
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   ö
   Gaps
  Gaps
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   ;
0
  79.4%; Score 127; DB 2; Length 34; 83.9%; Pred. No. 1e-09; ive 1; Mismatches 4; Indels
  Length 34;
   Indels
  Query Match 79.4%; Score 127; DB 2; Best Local Similarity 83.9%; Pred. No. 1e-09; Matches 26; Conservative 1; Mismatches 4
  1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31
  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
SVSEIQLMHDXGKHLNSMERVEWLRKKLQDV 31
   FEATURE:

COTHER INFORMATION: modified human PTH
US-09-843-221A-17
   ; OTHER INFORMATION: modified human PTH US-09-843-221A-18
   Sequence 17, Application US/09843221A
Patent No. 6756480
  TYPE: PRT
ORGANISM: Artificial Sequence
  ORGANISM: Artificial Sequence
  Query Match 79.4
Best Local Similarity 83.9
Matches 26; Conservative
   RESULT 5
US-09-843-221A-17
   g
a
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Gaps

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Indels

3,

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Best Local Similarity 80.6%; Pred. No. 1e-09; Matches 25; Conservative 3; Mismatches
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
  : 35 amino acids amino acids
  ropology:
  LENGTH:
   ò
   g
   рp
         ; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34) -. (34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163
   ö
   NAME/KEY: Modified-site

LOCATION: 35
COTHER INFORMATION: /note= "Where "Xaa" is selected
COTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
COTHER INFORMATION: amide, or the sequence of amino acids comprising
COTHER INFORMATION: residues 35-84 of PTH."
   Gaps
  RESULT 9
US-08-14-551B-52
Sequence 52, Application US/08142551B
Sequence 52, Application US/08142551B
Setent No. 5814603
GAPPLICANT: Oldenburg, Kevin R.
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: Jacandria
   Query Match 79.4%; Score 127; DB 2; Length 34; Best Local Similarity 83.9%; Pred. No. 1e-09; Matches 26; Conservative 1; Mismatches 4; Indels
  Length 35;
   COUNTRY: us

ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IRM PC compatible
CURRENT APPLICATION UNDER: US/08/142,551B
FILING DATE: 25-OCT -1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT -1992
ATTORNEY/ARCH INFORMATION:
NAME: Swissy Gerald F:
TELECOMMUNICATION INFORMATION:
NAME: Swissy Gerald F:
TELECOMMUNICATION INFORMATION:
TELEC
   79.4%; Score 127; DB 1;
  :|||||||| | ||||| || SVSEIQLMHINKGKHLNSMERVEWLRKKLLQDV 31
  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
  LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
   Query Match
   g
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0
   | IUTCLUCAS: UNKNOWN
| MOLECULE TYPE: protein
| FEATURE: | Modified-site
| NAME/KEY: Modified-site
| NAME/KEY: Modified-site
| OFFIER INFORMATION: from the group consisting of Hol, Ho, a homoserine
| OTHER INFORMATION: from the sequence of amino acids comprising
| OTHER INFORMATION: residues 15-84 of PTH."
   Gaps
   .
0
  RESULT 10
US-08-142-551B-56
US-08-142-551B-56
US-08-142-551B
Patent No. 5914603
GENERAL INPORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold B.
TITLE OF INVERTION: COMPOUNDS WITH PTH ACTIVITY AND ITTLE OF INVERTION: COMPOUNDS WITH PTH ACTIVITY AND STREET: 699 PRINCES: 13 CORRESPONDENCES: 13 COUNTRY: US
COUNTRY: Usuria, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: ALexandria Street
STATE: Virginia COUNTRY: US
COUNTRY: US
COUNTRY: US
SOFTWARE: PEADABLE FORM: PC-DOS/MS-DOS
SOFTWARE: PEADABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC COMPATION
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEACHLIN Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US 08/077,296
FILING DATE: 13-UN-1993
PRICH APPLICATION NUMBER: US 07/898,219
FILING DATE: 11-UN-1993
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1992
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1993
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1993
PRICH APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1993
PRICH APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1993
PRICH APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1993
PRICH APPLICATION NUMBER: US 07/898,6677
FELEPHONE: (415) 844-7400
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 844-7400
TELEPHONE: (415) 844-8275
INPORMATION POR RESULES CONTACTORS
INPORMATION POR RESULES POR PORTACTORS
INPORMATION POR RESULES POR PORTACTORS
INPORMATION POR RESULES POR PORTACTORS
I
   Query Match 79.4%; Score 127; DB 1; Length 35; Best Local Similarity 80.6%; Pred. No. 1e-09; Matches 25; Conservative 3; Mismatches 3; Indels
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
```

```
APPLICANT: Morley, Paul
APPLICANT: Morley, Paul
APPLICANT: Morgebauer, Witcold
APPLICANT: Ross Virginia
APPLICANT: Ross Virginia
APPLICANT: Wilfield, James
APPLICANT: Wilfield, James
APPLICANT: Willick, Gordon E.
TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 6
CORRESSED: NIXON & VANDERHYE, P.C.
STREET: 1100 New York Avenue, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READBLE FORM:
MEDIUM TYPE: IDOPPY disk
COMPUTER: IBN PC compatible
FORM:
COMPUTER: IBN PC COMPATIBLE FORM:
COMPUTER: IBN PC COMPATIBLE COMPATIBLE FORM:
COMPUTER: IBN PC COMPATIBLE COMPATIBLE FORM:
COMPUTER: IBN PC COMPATIBLE COMPATIBLE FORM:
COMPATIBLE THE PC COMPATIBLE FORM:
COMPATIBLE THE PC COMPATIBLE COMPATIBLE FORM:
COMPATIBLE THE PC COMPATIBLE FORM:
COMPATIBLE THE FORM:
COMPATIBLE THE PC COMPATIBLE FORM:
COMPATIBLE
   Length 31;
   4; Indels
  Score 125; DB 1;
Pred. No. 1.7e-09;
1; Mismatches 4;
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
  1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,647C
FILING DATE: August 2, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CTAMEORG, ARCHULE R.
REGISTRATION NUMBER: 25,327
112 Kent Street, Suite 770,
  US/08/262,495C
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/262,49:
FILING DATE:
CLASSIFICATION S30
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE:
FILING DATE:
FILENCHIPPORMATION:
TELEPHONE: 630
TELEPHONE: 613)-237-6900
TELEPHONE: (613)-237-6900
TELEPHONE: (613)-237-6900
TELEPHONE: (613)-237-6045
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                           CITY: Ottawa
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  US-08-691-647C-1
; Sequence 1, Application US/08691647C
; Patent No. 5955425
   Query Match
78.1%;
Best Local Similarity 83.9%;
Matches 26; Conservative
  TOPOLOGY: linear
MOLECULE TYPE: peptide
  amino acid
   GENERAL INFORMATION:
  US-08-262-495C-3
  ઠે
  d
   ö
   Gaps
   Sequence 8, Application US/09044536A
Patent No. 6025467
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: AKKGAWA, Shizue
APPLICANT: TAKETOMI, Shigehisa
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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   Query Match 78.8%; Score 126; DB 2; Length 34; Best Local Similarity 83.9%; Pred. No. 1.4e-09; Matches 26; Conservative 1; Mismatches 4; Indels
  Sequence 3, Application US/08262495C
Patent No. 5556940
GENERAL INFORMATION:
APPLICANT: WILLICK, Gordon E.
APPLICANT: WHITFIELD, James F.
APPLICANT: SUREWICZ, Witold
APPLICANT: SUREWICZ, Witold
APPLICANT: NEUGENBAUER, Witold
TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/044,536A

FILING DATE: 19-MAR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/66,871

APPLICATION NUMBER: 08/66,871

FILING DATE: 12-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN, David G

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 46509-DIV

TELECOMMUNICATION NUMBER: 46509-DIV

TELECOMMUNICATION INFORMATION:

TELEFRAX: (617)523-3400

INFORMATION EN GIONO: 8:

SEQUENCE CRARACTERISTICS:

LENGTH: 34 main acids
  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kirby, Eades, Gale, Baker
  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  NAME/KEY: partial peptide
  130 Water Street
  ADDRESSEE: DIKE, BRONS
STREET: 130 Water Stre
CITY: BOSTON
STATE: Massachusetts
COUNTRY: US
   MOLECULE TYPE: peptide FEATURE:
  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
  1..34
  ;
US-09-044-536A-8
   US-09-044-536A-8
  RESULT 12
US-08-262-495C-3
   COUNTRY:
   g
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Gaps

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  Gaps
   APPLICANT: Wolfeld No. 0595425;

Sequence 6, Application US/08691647C

Sequence 6, Application US/08691647C

Sequence 6, Application US/08691647C

Sequence 6, Application US/08691647C

APPLICANT: Wolfeld James

APPLICANT: Nougebouer, Witold APPLICANT: Ross, Virginia

APPLICANT: Willick, Gordon E.

TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE, P.C.

STREET: 1100 New YORK Avenue, 8th Floor
  Query Match 78.1%; Score 125; DB 1; Length 31; Best Local Similarity 83.9%; Pred. No. 1.7e-09; Matches 26; Conservative 1; Mismatches 4; Indels
  Length 31;
  Score 125; DB 1; Length 31 Pred. No. 1.7e-09; 1; Mismatches 4; Indels
   1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
  CITY: Alington
STATE: Virginia
CONTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/08/691,647C
FILING DATE: August 2, 1996
CLASSIFICATION: 514
   ATTORNEY/AGENT INFORMATION:
NAME: Crawfcod, Arthur R.
REGISTRATION NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 1339-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4005
TELEFAX: (703) 816-4100
REFERENCE/DOCKET NUMBER: 1339-5
TELECOMMUNICATION:
TELEPHONE: (703) 816-4005
TELEFAX: (703) 816-4100
   Query Match
Best Local Similarity 83.9%;
Matches 26; Conservative 1
  TELEFAX: (703) 816-4100
TELEX: N/A
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids TYPE: amino acid TYPE: amino acid TYPE: alinear
   LENGTH: 31 amino acids

TYPE: amino acids

TOPOLOGY: cyclic

MOLECULE TYPE: protein
US-08-691-647C-6
   ) MOLECULE TYPE: protein US-08-691-647C-1
  g
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Gaps
  GENERAL INFORMATION:

APPLICANT: Jean-Rene, Barbier
APPLICANT: Neugebauer, Witcold
APPLICANT: Neugebauer, Witcold
APPLICANT: Neugebauer, Witcold
APPLICANT: Neugebauer, Witcold
APPLICANT: Naillick, Gordon E.
TITLE OF INVENTION: PRATHYROID HORMONE ANALOGUES FOR THE
TITLE OF INVENTION: TREATHENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6110892th Glebe Rd. 8th floor
CITY: ALINGTON OF COMPATIBLE
COMPTER: USA
COUNTRY: USA
COUNTRY: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPTER READABLE FORM:
MEDIUM TYPE: DETECTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/904,760B
FILING DATE: 01-AUG-1997
CLASSIFICATION NUMBER: 06/691,647
FILING DATE: 02-AUG-1996
ATORING ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 25,327
REGISTRATION NUMBER: 25,327
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REFERENCE/DOCKET NUMBER: 25,327
REGISTRATION   ö
  Length 31;
  Query Match 78.1%; Score 125; DB 2; Length 31 Best Local Similarity 83.9%; Pred. No. 1.7e-09; Matches 26; Conservative 1; Mismatches 4; Indels
  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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  Search completed: November 21, 2005, 16:16:21 Job time : 33 secs
  Sequence 1, Application US/08904760B
Patent No. 6110892
GENERAL INFORMATION:
   TOPOLOGY: linear
MOLECULE TYPE: protein
RESULT 15
US-08-904-760B-1
   US-08-904-760B-1
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Gaps . 0

1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

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US-10-361-928-5
FEATURE:
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  162, App
163, App
21, Appl
22, Appl
27, Appl
165, App
27, Appl
  Sequence 6, Appli
Sequence 5, Appli
   November 21, 2005, 16:15:23 ; Search time 110.5 Seconds (without alignments) 117.219 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
  US-09-843-221A-17
US-09-843-221A-18
US-09-843-221A-162
US-09-999-608-17
US-09-999-608-18
US-09-999-608-18
US-10-899-008-162
US-10-899-007-17
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-10-839-037-165
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Maximum Match 100%
Listing first 45 summaries
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160
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   Title:
Perfect score:
   Scoring table:
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   Minimum DB
Maximum DB
  Searched:
   Sequence:
  Run on:
  Result
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  Sequence 1, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 16, Appl
Sequence 16, Appl
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Sequence 17, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 175, Appl
   3, Appli
1, Appli
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3, Appli
5, Appli
6, Appli
16, Appli
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6, Appli
   Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; Publication No. US20030144209A1
; GRERRAL INFORMATION:
   APPLICANT: TAKASU, HISASHI
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GRADELLA, THOMAS J.
   TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: AMALOGS
; FILE REPERENCE: 6069-4630002
; CURRENT FILING DATE: 2003-02.1
; PRIOR PLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR PLICATION NUMBER: 60/110,152
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PARENTIN VOY: 2.1
   Gaps
  Gequence 5, Application US/10361928
Publication No. US20030144209A1
GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
APPLICANT: GARDELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMALOGS
FILLE REPERENCE: 06609.4630002
CURRENT APPLICATION NUMBER: US/10/361,928
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US-10-892-025-2
US-11-040-557-20
US-11-040-557-20
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US-09-858-0478-6
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
   NAME/KEY: MOD_RES
LOCATION: (1)
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Sequence 162, Application US/09843221A

| Sequence 162, Application US/09843221A
| CENERAL INFORMATION:
| Publication No. US20030039654A1
| CENERAL INFORMATION:
| APPLICANT: KOSTENUIK,
| APPLICANT: LACEY, DAVID LEE
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HC
| TITLE OF INVENTION: NUMBER: 05/09/843,221A
| CURRENT FILING DATE: 2001-04-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2000-06-28
| PRIOR FILING DATE: 2000-06-28
| PRIOR FILING DATE: 2000-06-38
| PRIOR FILING DATE: 2000-04-26
| PRIOR FILING DATE: 2000-04-36
| PRIOR FILING DATE: 2000-04-37
| NUMBER OF SEQ ID NOS: 170
| SOFTWARE: PRIOR P
  FEATURE:
COTHER INFORMATION: Preferred embodiments - PTH
NAME/KEX: MAME/KEX:
LOCATION: (34)
COTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162
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  ö
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Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels
   Length 34;
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79.4%; Score 127; DB 3;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4.
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
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PRIOR PILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
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US-09-843-221A-18
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; Sequence 163, Application US/09843221A
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ORGANISM: Artificial Sequence
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  US-09-843-221A-18
Sequence 18, Application US/09843221A
Sequence 18, Application US/09843221A
PUBLICATION OF US20030039654A1
SERREAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
   OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
   ö
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   Gaps
   Gaps
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0
   Match 80.0%; Score 128; DB 4; Length 34; Local Similarity 87.1%; Pred. No. 2.1e-09; les 27; Conservative 0; Mismatches 4; Indels
  Query Match 79.4%; Score 127; DB 3; Best Local Similarity 83.9%; Pred. No. 2.8e-09; Matches 26; Conservative 1; Mismatches 4
   GENERAL INPOGRATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: WODULATORS OF RECEPTORS FC
TITLE OF INVENTION: WOLLATOR DAVID LEE
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR PILING DATE: 2001-04-66
PRIOR PILING DATE: 2000-62-86
PRIOR PILING DATE: 2000-62-87
PRIOR FILING DATE: 2000-64-87
PRIOR FILING DATE: 2000-64-87
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PALENTIN VETSION 3.1
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   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
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                   CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 09/47,800
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/110,152
PRIOR APPLICATION NUMBER: 60/110,152
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
ENGTH: 34
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US-09-843-221A-17
  US-09-843-221A-17; Sequence 17, Application US/09843221A; Publication No. US20030039654A1; GENERAL INFORMATION:
  NAME/KEY: MOD_RES

LOCATION: (1)
OTHER INFORMATION: Desamino Ala
US-10-361-928-8
   TYPE: PRT
ORGANISM: Artificial Sequence
  ORGANISM: Homo sapiens
FEATURE:
   Query Match
Best Local S:
Matches 27
```

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g

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GENERAL INFORMATION:
APPLICANT: KOSTEMUIK, PAUL
APPLICANT: GEGG COLIN V.
APPLICANT: KINSTLER, OLAF BORIS
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: BORDER: US/09/999,608
TITLE REFERENCE: A. 2002-03-11
FILE REFERENCE: 2001-04-26
CURRENT APPLICATION NUMBER: US 60/243,221
PRIOR APPLICATION NUMBER: US 60/24,860
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
   APPLICANT: KOSTENIIK, PAUL
APPLICANT: GEGG, COLIN V.
APPLICANT: GAGGINSTIN ANTHONY
APPLICANT: JAROSINSKI, MARK ANTHONY
APPLICANT: KINSTLER, OLAF BORIS
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
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  ö
  Length 34;
  Indels
   Query Match
79.4%; Score 127; DB 3;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4;
  1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31
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   FILE REFERENCE: A-665C
CURRENT APPLICATION NUMBER: US/09/999,608
CURRENT FILING DATE: 2002-03-11
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-00-26
PRIOR PELICATION NUMBER: US 60/266,673
PRIOR FILING DATE: 2001-02-06
PRIOR PELICATION NUMBER: US 60/214,860
PRIOR PILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: US 60/200,053
PRIOR APPLICATION NUMBER: US 60/200,053
PRIOR PILING DATE: 2000-06-28
                                     1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
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   ; Sequence 162, Application US/0999608; Publication No. US20050124537A1; GENERAL INFORMATION:
  Sequence 18, Application US/09999608
Publication No. US20050124537A1
GENERAL INFORMATION:
  SOFTWARE: Patentin version 3.2
SEQ ID NO 162
LENGTH: 34
  ORGANISM: Artificial Sequence
  US-09-999-608-162
  US-09-999-608-18
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  셤
  g
  ઠે
  APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LACEY: DAVID LEE
TITLE OF INVENTION: MODILATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 163
LENGTH: 34
   US-UY-YYY-6UB-I/

| Sequence 17, Application US/0999608
| Publication No. US20050124537A1
| GENERAL INFORMATION:
| APPLICANT: GEGG, COLIN V.
| APPLICANT: GEGG, COLIN V.
| APPLICANT: GEGG, COLIN V.
| APPLICANT: MARK ANTHONY
| APPLICANT: MINSTLER, OLAF BORIS
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PROFICE A 665C
| CURRENT FILING DATE: 2002-03-11
| PRIOR PILING DATE: 2001-04-26
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| PRIOR PILING DATE: 2000-04-27
| NUMBER OF SEQ ID NOS: 193
| SOFTWARE: PATENTIN VERSION 3.2
| SEQ ID NO 17
| LENGTH: 34
  NAME/KEY: misc_feature; LOCATION: (34)...(34
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   79.4%; Score 127; DB 3; Length 34; 83.9%; Pred. No. 2.8e-09; iive 1; Mismatches 4; Indels
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  4; Indels
  Query Match 79.4%; Score 127; DB 3; Best Local Similarity 83.9%; Pred. No. 2.8e-09; Matches 26; Conservative 1; Mismatches 4
   OTHER INFORMATION: Preferred embodiments - PTH
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
   CTHER INFORMATION: modifiled human PTH US-09-999-608-17
  ORGANISM: Artificial Sequence
   TYPE: PRT
ORGANISM: Artificial Sequence
Publication No. US20030039654A1
GENERAL INFORMATION:
  Best Local Similarity 83.9
Matches 26, Conservative
  US-09-999-608-17
   Query Match
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UNCS-10-839-037-18
Sequence 18, Application US/10839037
Sequence 18, Application US/10839037
Sequence 18, Application No. US20040214996A1
Sequence 18, Application No. US20040214996A1
SEQUENCE INFORMATION:
APPLICANT: LIU, CHUMN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC
TITLE OF INVENTION: NELATED PROTEIN
TITLE OF INVENTION: NUMBER: US/10/839, 037
CURRENT PILING DATE: 2004-05-04
FRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PELING DATE: 2000-04-27
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SEQUENCE FILING DATE: 2000-04-27
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  Gaps
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   ó,
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TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT PILIANG DATE: 2004-05-04
PRIOR APPLICATION NUMBER: US/10/843,221A
PRIOR APPLICATION NUMBER: US/09/843,221A
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ORGANISM: Artificial Sequence
   TYPE: PRT
ORGANISM: Artificial Sequence
  RESULT 13
US-10-839-037-162
  US-10-839-037-18
   SEQ ID NO 17
LENGIH: 34
   ò
   ò
  a
   g
   RESULT 10

US-09-999-608-163

Sequence 163, Application US/0999608

Publication No. US20050124537A1

GENERAL INFORMATION:
APPLICANT: GEGG, COLIN V.
APPLICANT: HOMONE-RELATED PROTEIN
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: MODULATORS OF RECEPTORS
TITLE OF INVENTION: MODULATORS OF RECEPTORS
TITLE OF INVENTION: MODULATORS OF RECEPTORS
FILMS APPLICATION NUMBER: US 60/266,673
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2000-06-28
SEQ ID NO 163
SEQ ID NO 163
LENGTH: 34
   US-10-839-037-17
Sequence 17, Application US/10839037
Sequence 17, Application US/10839037
Sequence 17, Application No. US20040214996A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
  i LOCATION: (14) ... (14); OTHER LINFORMATION: Optional linker and Fc domain attached at the C-terminus (18-09-999-608-163)
  NAME/KEY: misc_feature

1 LOCATION: (34)

1 OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-999-608-162
  ö
  ö
  Gaps
  Gaps
  ö
   Length 34;
  Length 34;
   Query Match
79.4%; Score 127; DB 3; Length 34
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels
  4; Indels
   Query Match 79.4%; Score 127; DB 3; Best Local Similarity 83.9%; Pred. No. 2.8e-09; Matches 26; Conservative 1; Mismatches 4
   OTHER INFORMATION: Preferred embodiments - PTH FEATURE:
   FEATURE:
OTHER INFORMATION: Preferred embodiments - PTH
   1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
   ORGANISM: Artificial Sequence
              TYPE: PRT
ORGANISM: Artificial Sequence
  NAME/KEY: misc feature
  g
```

ö

```
Sequence 21, Application US/10892025

Publication No. US20050065071A1

GENERAL INFORMATION:

APPLICANT: Whitfield, James F

TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID

TITLE OF INVENTION: HORMONE FOR THE TREATHENT OF CONDITIONS CHARACTERIZED BY

TITLE OF INVENTION: HORMONE FOR THE TREATHENT OF CONDITIONS CHARACTERIZED BY

TITLE OF INVENTION: HYPERENCLIFERATIVE SKIN CELLS

TITLE OF INVENTION: HYPERENCLIFERATIVE SKIN CELLS

CURRENT APPLICATION NUMBER: US/10/892,025

CURRENT PILING DATE: 2003-07-15

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 31
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; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-10-839-037-163
   ö
   Gaps
  NAME/KEY: VARIANT LOCATION: 12 LOCATION: 13 Selected from the group consisting of Lys, Orn, OTHER INFORMATION: 18 Selected from the group consisting of Lys, Orn, OTHER INFORMATION: Glu, Asp, Cys, and homocysteine
   CTHER INFORMATION: Y; where Y is X, His-X, His-Asn-X, or CTHER INFORMATION: His-Asn-Phe-X; X is OR or NHR; and R is hydrogen OTHER INFORMATION: or a linear or branched chain alkyl, acyl or aryl US-10-892-025-21
   OTHER INFORMATION: NHR; where R is hydrogen or a linear or branched OTHER INFORMATION: chain alkyl, acyl or aryl group
   ö
  ö
  Length 31;
   Length 34;
   Indels
  Indels
  Query Match 78.8%; Score 126; DB 5; Best Local Similarity 83.9%; Pred. No. 3.5e-09; Matches 26; Conservative 1; Mismatches 4
  Query Match

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Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4
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   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
  Search completed: November 21, 2005, 16:34:42 Job time : 111.5 secs
  TYPE: PRT
ORGANISM: Homo sapien
  NAME/KEY: SITE
LOCATION: 1
  NAME/KEY: SITE
  LOCATION:
   FEATURE:
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   원
  ò
  Sequence 163, Application US/10839037

| Sequence 163, Application US/10839037
| Publication No. US20040214996A1
| Publication No. US20040214996A1
| GENERAL INFORMATION:
| APPLICANT: LACEY, DAVID LEE
| TITLE OF INVENTION: MOULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE APPLICANTON: RELATED PROTEIN
| FILE REFERENCE: A-665B
| CURRENT APPLICATION NUMBER: US/10/839, 037
| CURRENT FILING DATE: 2004-05-04
| PRIOR APPLICATION NUMBER: 60/214,860
| PRIOR FILING DATE: 2001-02-06
| PRIOR FILING DATE: 2000-04-27
| PRIOR APPLICATION NUMBER: 60/214,860
| PRIOR FILING DATE: 2000-04-27
| NUMBER OF SEQ ID NOS: 170
| SEQ ID NO 163
| LENGTH: 34
| LENGTH: 34
   GENERAL INCREATION

APPLICANT: KOSTENUIK, PAUL

APPLICANT: LACY: DAVID LES

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

FILE REFRENCE: A-6658

CURRENT APPLICATION NUMBER: US/10/839,037

CURRENT APPLICATION NUMBER: US/09/843,221A

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2000-06-28

  NAME/KEY: misc_feature

1 LOCATION: (34)...(34)...

2 OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-10-839-037-162
   ö
   Gaps
   ö
   Length 34;
   4; Indels
  Score 127; DB 4;
Pred. No. 2.8e-09;
  FEATURE: OTHER INFORMATION: Preferred embodiments - PTH
   OTHER INFORMATION: Preferred embodiments - PTH
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
   1; Mismatches
                       Sequence 162, Application US/10839037
Publication No. US20040214996A1
GENERAL INFORMATION:
  Query Match
Best Local Similarity 83.9%;
Matches 26; Conservative
   ORGANISM: Artificial Sequence
  ORGANISM: Artificial Sequence
  NAME/KEY: misc_feature
  US-10-839-037-163
   LENGTH: 34
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2

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November 21, 2005, 16:16:29; Search time 4 Seconds (without alignments)
8.756 Million cell updates/sec
  Published Applications AA New:*

1: /cgn2_6/ptodata/3/pubpaa/US10.NEW FUB.pep:*
2: /cgn2_6/ptodata/3/pubpaa/US06_NEW_FUB.pep:*
3: /cgn2_6/ptodata/3/pubpaa/US07_NEW_FUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_FUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_FUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
   1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
  Total number of hits satisfying chosen paramete'rs:
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   8323 seqs, 1129788 residues
   - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
   US-09-475-158A-3
160
   Title:
Perfect score:
  Scoring table:
   Database :
   OM protein
  Sequence:
  Searched:
   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result |       | *<br>Query |              |    |                    |                   |
|--------|-------|------------|--------------|----|--------------------|-------------------|
|        | Score | Match      | Match Length | BB | ID                 | Description       |
|        | 47    | 29.4       | 263          | ч  | US-10-512-184-29   |                   |
|        | 46.5  | 29.1       | 317          | 7  | US-11-082-389-28   | Sequence 28, Appl |
|        | 44    | 27.5       | 157          | Н  | US-10-957-569-64   | 64,               |
|        | 44    | 27.5       | 1213         | 7  | US-11-074-176-256  | 256,              |
|        | 44    | 27.5       | 1493         | 7  | US-11-004-057-21   | 21,               |
|        | 42    | 26.2       | 28           | П  | US-10-939-890-474  | 474,              |
|        | 42    | 26.2       | 28           | -  | US-10-939-890-726  | 726,              |
|        | 40    | 25.0       | 28           | Н  | US-10-939-890-464  | 464, 7            |
|        | 40    | 25.0       | 28           | ~  | US-10-939-890-720  | 720,              |
|        | 40    | 25.0       | 28           | ч  | US-10-939-890-723  | 723,              |
|        | 40    | 25.0       | 1493         | 7  | US-11-004-057-4    | 4, A              |
|        | 39    | 24.4       | 120          | 7  | US-11-077-978-7    | 7                 |
|        | 39    | 24.4       | 360          | 7  | US-11-084-408-3    | Α,                |
|        | 39    | 24.4       | 386          | -  | US-10-131-826A-340 | 340               |
|        | 39    | 24.4       | 562          | 7  | US-11-065-943-20   | 20,               |
|        | 39    | 24.4       | 562          | 7  | US-11-065-943-22   | 22,               |
| _      | 39    | 24.4       | 562          | 7  | US-11-065-943-24   | 24,               |
| _      | 39    | 24.4       | 562          | 7  | US-11-065-943-26   | 26,               |
| o      | 39    | 24.4       | 562          | 7  | Ξ                  | 7                 |
| _      | 39    | 24.4       | 562          | 7  | US-11-065-943-30   | 30,               |
|        | 39    | 24.4       | 562          | 7  | US-11-065-943-32   | 32,               |
|        | 39    | 24.4       | 562          | 7  | US-11-065-943-34   | 34,               |
|        | 39    | 24.4       | 562          | 7  | US-11-065-943-36   | 36,               |
|        | 39    | 24.4       | 562          | 7  | US-11-065-943-38   | 38,               |
|        | 38.5  | 24.1       | 346          | 7  | US-10-967-648A-10  | Sequence 10, Appl |
|        |       |            |              |    |                    |                   |

| Sequence 9, Appli | Sequence 78, Appl | Seguence 94, Appl | Seguence 99, Appl | Sequence 4, Appli | Sequence 10, Appl | Sequence 32, Appl | Sequence 6, Appli | Sequence 2, Appli | Sequence 3, Appli | Sequence 24, Appl | Sequence 16, Appl | Sequence 8, Appli | Sequence 12, Appl | Seguence 33, Appl | Sequence 68, Appl | Seguence 45, Appl | Sequence 46, Appl | Sequence 37, Appl | Sequence 8, Appli |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| US-10-789-273-9   | US-11-074-176-78  | US-10-131-826A-94 | US-10-467-962B-99 | US-10-789-273-4   | US-10-789-273-10  | US-11-144-248-32  | US-10-997-201A-6  | US-11-077-978-2   | US-11-077-978-3   | US-11-144-248-24  | US-11-144-248-16  | US-10-789-273-8   | US-10-789-273-12  | US-10-721-763-33  | US-10-510-386-68  | US-11-144-248-45  | US-11-144-248-46  | US-10-972-587-37  | US-10-499-715-8   |
| н                 | 7                 | н                 | Н                 | н                 | н                 | 7                 | Н                 | 7                 | 7                 | 7                 | 7                 | г                 | 7                 | н                 | П                 | 7                 | 7                 | п                 | ч                 |
| 121               | 384               | 429               | 828               | 138               | 98                | 98                | 102               | 121               | 121               | 122               | 125               | 138               | 138               | 139               | 401               | 470               | 470               | 114               | 336               |
| 23.8              | 23.8              | 23.8              | 23.8              | 23.4              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 23.1              | 22.8              | 22.8              |
| 38                | 38                | 38                | 38                | 37.5              | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 37                | 36.5              | 36.5              |
| 9                 | _                 | 00                | ტ                 | 0                 | -                 | 2                 | m                 | 4                 | S                 | 9                 | 7                 | 80                | 6                 | 0                 | =                 | 2                 | 2                 | 4                 | ις:               |

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Sequence 29, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
TITLE OF INVENTION: resistance against fungi
TITLE OF INVENTION: 1010101

CURRENT APPLICATION NUMBER: US/10/512,184

CURRENT FILING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29

LENGTH: 263
  .;
7
   CTHER INFORMATION: Description of Artificial Sequence: scFv SPIII7; CTHER INFORMATION: with specificity against Fusarium ssp.; originates; OTHER INFORMATION: from Mus musculus.
  Gaps
  16;
  29.4%; Score 47; DB 1; Length 263; 29.3%; Pred. No. 2; tive 9; Mismatches 4; Indels
  2 VSEIQLMHGGGGGL---NSME-----RVEWLRK 26
  ALIGNMENTS
  TYPE: PRT
ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity 29.3'
Matches 12; Conservative
  FEATURE:
  RESULT 2
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RESULT 5

(Sequence 21, Application US/11004057)

(Sequence 21, Application US/11004057)

(Sequence 21, Application No. US20050244846A1)

(SEGNERAL INFORMATION:

(APPLICANT: USANATION:

(APPLICANT: USANATION:

(APPLICANTION:

(APPLICANT: APPLICANTION:

(CURRENT APPLICATION NUMBER: US/11/004,057)

(CURRENT APPLICATION NUMBER: US/11/004,057)

(CURRENT PILING DATE: 2004-12-02)

(CURRENT PILING DATE: 2000-05-10)

(MUMBER OF SEQ ID NOS: 21)

(SOFTWARE: PATCHIN UVET: 2.0)

(SOFTWARE: PATCHIN UVET: 2.0)
   ۲,
  ä
   7; Indels 18; Gaps
  Gaps
  APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: Malliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
APPLICANT: Peril, Andrea Azcarate
TILE OF INVENTION: Nucleic Acid Sequences Encoding
TILE REPRENCE: 5051-694
TILE REPRENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-03-08
NUMBER OF SEQ ID NOS: 381
SEQ ID NO 256
LENGTH: 1213
  18;
   ch 27.5%; Score 44; DB 7; Length 1493; 1 Similarity 27.5%; Pred. No. 32; 11; Conservative 4; Mismatches 7; Indels 1
  Query Match 27.5%; Score 44; DB 7; Length 1213; Best Local Similarity 25.6%; Pred. No. 26; Matches 11; Conservative 8; Mismatches 6; Indels 1
  :::: || || :|: || 873 ISLRVPHGGGGIVQDVKVYTREAGDELSPGVNTWVRVYIAQKR 915
   ------GLNSMERVEWLRKK 27
   10 GGGGGLN-----SMERVEWLRKKLQDV 31
   Sequence 474, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
  ; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-256
  APPLICANT: Satto, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Fan, Hong APPLICANT: Khurana, Sudha APPLICANT: Linder, Karen E.
   3 SEIQLMHGGGG-----
   ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-004-057-21
   Query Match
Best Local S
Matches 11
   LENGTH:
  RESULT 6
   ò
  g
  ò
   В
   Sequence 64, Application US/10957569
Fublication No. USZ0050246785A1
GENERAL INFORMATION:
TUTLE COOK, ZAIHONG et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION WINBER: US 10/950,321
PRIOR FILING DATE: 2004-09-23
NUMBER OF SEQ ID NOS: 64
SSO ID NO 64
ILENGTH: 157
  1;
   ÷
CURRENT FILING DATE: 2005-03-16

PRIOR PEDLICATION NUMBER: US 09/603024

PRIOR FILING DATE: 2000-06-23

PRIOR PELLING DATE: 1999-06-25

PRIOR PELLING DATE: 1999-06-25

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-01

PRIOR PELLING DATE: 1999-07-08

PRIOR PELLING DATE: 1999-07-08

PRIOR PELLING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1909-07-09

  Gaps
  Gaps
   ö
   Query Match 29.1%; Score 46.5; DB 7; Length 317; Best Local Similarity 41.4%; Pred. No. 2.8; Matches 12; Conservative 4; Mismatches 8; Indels 9
  Query Match 27.5%; Score 44; DB 1; Length 157; Best Local Similarity 50.0%; Pred. No. 2.9; Marches 8; Conservative 2; Mismatches 6; Indels
   86 VSEADIIIVGGGGYDS-----WLYGTLED 109
   2 VSEIQLMHGGGGGLNSMERVEWLRKKLQD 30
  ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-28
  ; Sequence 256, Application US/11074176; Publication No. US20050250135A1; GENERAL INFORMATION:
   ) ORGANISM: Arabidopsis thaliana US-10-957-569-64
  88 GGGGGSSSSRSRDWKK 103
  10 GGGGGLNSMERVEWLR 25
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RESULT 3 US-10-957-569-64

ò g US-11-074-176-256

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LOCATION: (28)...(28); OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker US-10-939-890-726
  APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
  Score 42; DB 1;
Pred. No. 0.86;
2; Mismatches
PRIOR FILING DATE: 2003-03
PRIOR FILING DATE: 2003-03
PRIOR PILING DATE: 2003-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 726
LENGTH: 28
   PRIOR PELICATION NUMBER: US 10/661,156
PRIOR PELING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2002-01-15
  CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
   OTHER INFORMATION: Synthetic peptide
   Sequence 464, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
   Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
  Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
  APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
  LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
   Query Match 26.2%;
Best Local Similarity 75.0%;
   ORGANISM: Artificial sequence
   Shrivastava, Ajay
  6; Conservative
  ::||||||
20 ILHGGGGG 27
   7 LMHGGGGG 14
   Fan, Hong
  Song, Bo
  NAME/KEY: MOD_RES
LOCATION: (1)...(1)
  FEATURE:
NAME/KEY: MOD_RES
  US-10-939-890-464
  APPLICANT:
APPLICANT:
APPLICANT:
   TYPE: PRT
   APPLICANT
   APPLICANT
   APPLICANT
   FEATURE:
  Matches
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   Gaps
   ö
  Ouery Match

26.2%; Score 42; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.86;
Matches 6; Conservative 2; Mismatches 0; Indels
  APPLICANT: SWENGO, KOLI E.

APPLICANT: SWENGO, KOLI E.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRIOR PELING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-13
PRIOR PELING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-01
SPIOR FILING DATE: 2003-01
SPIOR FILING DATE: 2003-01
SPIOR FILING DATE: 2003-03-01
SPIOR PILING DATE: 2003-03-01
SPIOR PILING DATE: 2003-03-01
SPIOR PILING DATE: 2003-03-01
SEQ ID NO 474
LENGTH: 28
  APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION WUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION UNMBER: US 10/661,156
                          Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
  US-10-939-890-726
Sequence 726, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
   Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
  APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
  OTHER INFORMATION: Library Isolate
  Pillai, Radhakrishna
  ORGANISM: Artificial Sequence
   Song, Bo
Swenson, Rolf E.
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20 ILHGGGGG 27
   7 LMHGGGGG 14
   Song, Bo
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APPLICANT:
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APPLICANT:
   APPLICANT:
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Gaps

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Length 28; 0; Indels Ή;

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Gaps
   Gaps
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   5
  Query Match 25.0%; Score 40; DB 1; Length 28; Best Local Similarity 57.1%; Pred. No. 1.6; Matches 8; Conservative 3; Mismatches 1; Indels
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NAMEXKEY: MOD RES
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COHER INVORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723
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   APPLICANT: SONG; HO
APPLICANT: SONG; HO
APPLICANT: VON WCONGY; Mathew A.
TITLE OF INVENTION: KDNE AND VEGF/KDR BINDING PEPTIDES
FILE REPRENCE: D6617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-05
PRIOR PRILING DATE: 2003-01-05
PRIOR FILING DATE: 2002-03-01
PRIOR PRI
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   Sequence 723, Application US/1093985; Publication No. US20050250700A1
is GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dadner, Robert C.
APPLICANT: Dadner, Robert C.
APPLICANT: Pansféleld, Daniel T.
APPLICANT: Pansféleld, Daniel T.
APPLICANT: Pansféleld, Daniel T.
APPLICANT: Pansféleld, Daniel T.
APPLICANT: Rangat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nunn, Adrian D.
APPLICANT: Pochon, Sibylle
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Sang, Bo
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OTHER INFORMATION: Synthetic peptide
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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US-10-939-890-720
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   APPLICANT: Song, Bo
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
APPLICANT: Won WICOMSKI, Mathew A.
ITILE OF INVENTION: KDR AND VEGFKUR BINDING PEPTIDES
FILE REFERENCE: D061,70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 60/440,411
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 464
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   Fan, Hong
Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylla
Ramalingam, Kondareddiar
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   Sequence 720, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
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   APPLICANT: Sato, Aaron K.
Sexton, Daniel J.
APPLICANT: Sexton, Daniel J.
Dransfield, Daniel T.
Dransfield, Daniel T.
Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Pusset, Philippe
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OTHER INFORMATION: ACETYLATION
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US-10-939-890-720
  g
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APPLICANT: A1-Shami, Amin APPLICANT: Spolski, Rosanne APPLICANT: Spolski, Rosanne APPLICANT: Spolski, Rosanne APPLICANT: Kelly, John APPLICANT: Kelly, John TITLE OF INVENTION: METHODS FOR USE OF TSLP AND AGONISTS AND ANTAGONISTS THEREOF FILE REPERBNCE: 4239-67781-02 CURRENT APPLICATION NUMBER: US/11/084,408 CURRENT APPLICATION NUMBER: US/11/084,408 PRIOR PLILING DATE: 2004-03-18 PRIOR PLILING DATE: 2004-03-23 PRIOR PLILING DATE: 2004-03-33 SOFTWARE: Patentin version 3.3 SEQID NOS: 11
   ä
  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT APPLICATION NUMBER: 00/049911
PRIOR APPLICATION NUMBER: 60/059911
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-09-17
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PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
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Pred. No. 34;
4; Mismatches 10; Indels
  4 EIQLMHGGGGGLNSMER--VEWLRKK 27
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  Stewart, Timothy A.
  Lenord, Warren J.
Pandey, Akhilesh
  Gerritsen, Mary E.
  Tumas, Daniel
Watanabe, Colin K
  Beresini, Maureen
   ; ORGANISM: Rattus norvegicus US-11-084-408-3
   Godowski, Paul J.
Gurney, Austin L.
  Desnoyers, Luc
Filvaroff, Ellen
  Sherwood, Steven
   Best Local Similarity 38.5
Matches 10; Conservative
   Smith, Victoria
  Goddard, Audrey
                               HUMAN SERVICES
  Gao, Wei-Qiang
   DeForge, Laura
  APPLICANT: Baker, Kevin P.
   Wood, William
   US-10-131-826A-340
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  ઠે
   OTHER INFORMATION: Variable heavy chain of humanized anti-p185HER2 antibody 4D5, OTHER INFORMATION: version 8
  GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

TITLE OF INVENTION: MEKKI PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
TITLE OF INVENTION: APOPTOSIS
FILE REFERENCE: CPI-042CPPC
CURRENT APPLICATION NUMBER: US/11/004,057
CURRENT PILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/9/403,075
PRIOR FILING DATE: 2000-05-10
  Sequence 7, Application US/11077978

Publication No. US20050244333A1

GENERAL INFORMATION:

APPLICANT: Yazaki, Paul J.

APPLICANT: Sharman, Mark A.

APPLICANT: Shaubitschek, Andrew A.

APPLICANT: Wu, Anna M.

TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof

FILE REFERENCE: 54435.8012.US01

CURRENT APPLICATION UNMBER: US/11/077,978

CURRENT FILING DATE: 2005-03-11

NUMBER OF SEQ ID NOS: 27

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; Sequence 3, Application US/11084408
; Publication No. USC050249712A1
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us-09-475-158a-3.rapbn

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US-11-065-943-20

US-11-065-943-20

Sequence 20, Application US/11065943

Beduence 20, Application US/11065943

Beduence 20, Application World Carologo Color Carologo Carolog
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
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Remaining Prior Application data removed - See File Wrapper or FALM.
NUMBER OF SEQ ID NOS: 550
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US-10-131-826A-340
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AAR22294 AAR74457 AAR74466 AAR74470

AAR21233 AAR21231

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Amino aci
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  New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   Parathyro
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  POTTS J T.
JUEPPNER H.
WO200039278-A2
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par par par

Human Human

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Compounds of the structure or formula S-(L) n-B, R.1-S-(L) n-R or S-(L) n-R are new. Si as an amino terminal signaling functional domain of parathyroid hormone (PTH); Lis a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R.1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:P which avoids the need for regular injections to treat osteoporosis
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   PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:P which avoids the need for regular injections to treat osteoporosis
  ö
New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammallan conditions characterized by decreases in bone mass.
  Gaps
  PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
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  Claim 7; Page 92-93; 119pp; English.
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(JUEP/) JUEPPNER H.
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Gaps

12;

31 86

Length 89;

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Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M are given in the specification (AAR21150-256, AAR23226 23.50 + AAR23522-59). Corresp. peptides created using residues 7-84 of bovine and porcine PTH are also claimed. All have mutations at positions 3, and/or 6, and/or 9 which result in surface side chains which are useful to modulate receptor binding and activity. They are useful as agonists and antagonists in the treatment of condi- tions or diseases involving PTH. The peptides are pref. pred0 by solid phase synthesis. See also AAR21257 (human generic). (Updated on 25-MAR-2003 to correct PA field.)
                high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of an amino acid sequence encoded by an expression cassette of the
   New modified parathyroid hormone analogues - useful in treating cancer, osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
invention relates to a novel expression cassette and methods for
  Score 103; DB 2; Length 84
Pred. No. 4.1e-05;
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Pred. No. 3.3e-05;
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  PTH; agonist; antagonist; receptor binding
  Strewler GJ;
  AAR21190 standard; protein; 84 AA
   Claim 15; Page 64; 86pp; English.
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(first entry)
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  23-JAN-1992
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   ;
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   Compounds of the structure or formula S-(L) n-B, R.1-S-(L) n-R or S-(L) n-R, are new, S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rares of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:P which avoids the need for regular injections to treat osteoporosis
  New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   Gaps
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   .,
8
   Novel expression cassette encoded amino acid sequence SeqID132.
  Length 31;
   Indels
  expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body.
  Score 116; DB 3; Lv
Pred. No. 3.9e-07;
); Mismatches 0;
  1 AVSEI----GGGGGGGGGLNSMERVEWLRKKLQDV 31
  31
  0; Mismatches
  Example 6; SEQ ID NO 132; 157pp; English
  Xia Y;
   Ą
  Luan P,
  Claim 7; Page 93; 119pp; English.
   ADG93251 standard; protein; 89
  71.6%;
77.1%;
   23-MAY-2003; 2003WO-US016643
  24-MAY-2002; 2002US-0383370P
  (first entry)
   27; Conservative
  Harley S, Williams JA,
  (REST-) RESTORAGEN INC.
   WPI; 2004-035128/03.
N-PSDB; ADG93252.
  Best Local Similarity
   HARL/) HARLEY S.
                            N-PSDB; AAA51730
  WO2003100021-A2
  Sequence 31 AA;
  Unidentified
   11-MAR-2004
  04-DEC-2003
   Synthetic.
```

ADG93251;

RESULT 4 ADG93251

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Query Match Matches

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Gaps

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Length 84;

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23-MAY-2003; 2003WO-US016647.
  24-MAY-2002; 2002US-0383484P.
  Query Match 63.6%;
Best Local Similarity 56.1%;
Matches 23; Conservative
06-MAY-2004 (first entry)
   (REST-) RESTORAGEN INC.
  Seo JS, Holmquist B;
   WPI; 2004-203533/19.
N-PSDB; ADJ87051.
  5 IGGGGGG--
   WO2004011599-A2.
  Sequence 91 AA;
  05-FEB-2004.
   Synthetic.
  Chimeric.
à
  The present invention describes a palladium complex-promoted hydrolytic polypeptide cleavage process, which selectively cleaves the polypeptide at a Cya-His cleavage site. The process comprises solubilising the polypebtide in a reaction mixture comprised of a palladium promoter dissolved in a high-concentration organic acid solvent. Also described: (1) a peptide purification process; and (2) a process for producing a peptide. The methods are useful for selectively cleaving the polypeptide at Cys-His cleavage site. The process provides a highly specific, conformationally independent, palladium promoted hydrolytic cleavage of polypeptides, including cleavage of relatively insoluble chimeric proteins in the form of includion bodies. The present sequence is used in the exemplification of the present invention.
   ï
   A palladium complex-promoted hydrolytic polypeptide cleavage process for cleaving the polypeptide at a Cys-His cleavage site, comprises solubilizing the polypeptide in mixture of a palladium promotor dissolved in organic acid solvent.
   Gaps
   14;
  palladium complex-promoted hydrolytic polypeptide cleavage;
Cys-His cleavage site; palladium promoter; chimeric protein;
inclusion body.
   Length 91;
   Score 103; DB 8; Length 91
Pred. No. 4.4e-05;
1; Mismatches 3; Indels
   31
   48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88
   5 IGGGGGG-------GGGLNSMERVEWLRKKLQDV
     AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
                              1 AVSEIGLMHNLGKHLNSMERVEWLRKKLODV 31
   Example 9; SEQ ID NO 19; 56pp; English.
   ADJ87052 standard; protein; 91 AA
  ADF90346 standard, protein, 91 AA
   Strydom D, Holmquist B;
   Chimeric protein SEQ ID NO:19.
  23-MAY-2003; 2003WO-US016468.
   Query Match
Best Local Similarity 56.1%;
Matches 23; Conservative 1
   24-MAY-2002; 2002US-0383488P.
  26-FEB-2004 (first entry)
  (REST-) RESTORAGEN INC.
   WPI; 2004-053266/05.
   N-PSDB; ADF90345.
  WO2003100015-A2.
   Sequence 91 AA;
   04-DEC-2003.
   Synthetic.
   ADF90346;
   ADJ87052
   Seo JS,
  RESULT 7
ADJ87052
ID ADJ8
XX
AC ADJ8
  RESULT 6
ADF90346
ADF
  ò
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Amino acid sequence of chimeric procein Trias Vg-56p-CH-ph(11-14).

Maino acid sequence of chimeric procein Trias Vg-56p-CH-ph(11-14).

My appliation promoter; formic acid; inclusion body; glucagon like peptide-1; which hormone releasing factor; one of the peptide-1; which hormone selected by the peptide-1; which hormone is demone; advanced by the peptide-1; which hormone is the peptide-
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Human parathyroid hormone analogue #65.
  ABJ10737
ID ABJ1
XX
  8
  셤
   ä
   The present invention describes a palladium complex-promoted hydrolytic polypeptide cleavage process, which selectively cleaves the polypeptide at a Cys-His cleavage site. The process comprises solubilising the polypeptide in a reaction mixture comprised of a palladium promoter dissolved in a high-concentration organic acid solvent. Also described: (1) a peptide purification process; and (2) a process for producing a peptide. The methods are useful for selectively cleaving the polypeptide of Cys-His cleavage site. The process provides a highly specific, conformationally independent, palladium promoted hydrolytic cleavage of polypeptides, including cleavage of relatively insoluble chimeric proteins in the form of inclusion bodies. The present sequence is used in the exemplification of the present invention.
  A palladium complex-promoted hydrolytic polypeptide cleavage process for cleaving the polypeptide at a Cys-His cleavage site, comprises solubilizing the polypeptide in mixture of a palladium promotor dissolved in organic acid solvent.
   Gaps
   14;
   palladium complex-promoted hydrolytic polypeptide cleavage; Cys-His cleavage site; palladium promoter; chimeric protein; inclusion body.
   Length 141;
  Indels
   --- GGGLNSMERVEWLRKKLQDV 31
   VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88
   63.6%; Score 103; DB 8; L4 56.1%; Pred. No. 6.8e-05; ive 1; Mismatches 3;
  Example 11; SEQ ID NO 21; 56pp; English
   ADF90348 standard; protein; 141 AA
  ABJ10769 standard; peptide; 34 AA.
   æ,
  Holmquist
  Chimeric protein SEQ ID NO:21
  23-MAY-2003; 2003WO-US016468.
  24-MAY-2002; 2002US-0383488P.
   (first entry)
   23; Conservative
  (REST-) RESTORAGEN INC
  WPI; 2004-053266/05.
  Strydom D,
  ---5555555I S
   Best Local Similarity
  N-PSDB; ADF90347
  Sequence 141 AA;
  WO2003100015-A2
   02-DEC-2002
   26-FEB-2004
   04-DEC-2003
  Synthetic.
   48
  ADF90348;
  Query Match
  Seo JS,
  Matches
  원
  XXXXXX
    셤
   ઠ
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   The present invention provides a number of parathyroid hormone (PTH) or parathyroid hormone-related protein (PTHrP) analogues. These act as PTHZ receptor agonists or antagonists and can be used in the treatment of disorders resulting from altered or excessive action of the PTH2 receptor, e.g. abnormal CNS functions, abnormal pancreatic functions, divergence from normal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or a hypothalmic disease. The present sequence is a peptide analogue of the invention
   New parathyroid hormone analogs, used for treating e.g. abnormal CNS or pancreatic functions, abnormal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or hypothalmic disease.
Human; parathyroid hormone; parathyroid hormone-related protein; PTH; PTHP; analogue; abnormal CNS function; maneral metabolism; male infertility; abnormal blood pressure; hypothalmic disease.
  Gaps
  ö
   Length 34;
  Indels
   Score 100; DB 3; L. Pred. No. 3.9e-05; L. Mismatches B;
  /label= OTHER
/note= "OTHER=cyclohexylalanine"
   /note= "OTHER=cyclohexylalanine"
  31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  SVSEIQXXXXXGKHLNSMERVEWLRKKLQDV
   /note= "C-terminal amide'
   label= OTHER
note= "OTHER=des-Asn"
   note= "OTHER=des-His"
  label= OTHER
note= "OTHER=des-Met"
   (SCRC ) SOC CONSEILS RECH & APPL SCI.
   Location/Qualifiers
  Ξ
   ABJ10737 standard; peptide; 34 AA.
  Claim 11; Page 39; 49pp; English.
  Rosenblatt
   label= OTHER
  'label= OTHER
   61.7%;
71.0%;
  99WO-US009521.
  98US-00072956
   Conservative
   note=
  /note=
  Dong ZX,
   WPI; 2000-038790/03.
   Local Similarity
   Sequence 34 AA;
   Modified-site
   Modified-site
  Modified-site
   Modified-site
   Modified-site
  Modified-site
  03-MAY-1999;
  05-MAY-1998;
   sapiens
  WO9957139-A2
   11-NOV-1999
   22;
   Synthetic.
  Chorev M,
   Query Match
  Ношо
   RESULT 10
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This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
  Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
  New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.
  Target peptide (PTH(1-38)) used in fusion protein construct.
  61.7%; Score 100; DB 2; Length 38;
larity 74.2%; Pred. No. 4.4e-05;
Conservative 1; Mismatches 7; Indels
  Fusion protein construct; isolation; purification; growth hormone releasing factor; glucagon-like peptide 1; parathyroid hormone; inclusion body; carbonic anhydrase.
  Rainer A;
  SVSEIQLMHNLGGHLNSMERVEWLRKKLQDV 31
  1 AVSEIGGGGGGGLNSMERVEWLRKKLODV 31
  Waelchli R,
  Example 101; Page 39; 92pp; English.
  AAR98958 standard; peptide; 38 AA.
  92GB-00026415.
92GB-00026859.
92GB-00026861.
93GB-00001691.
93GB-00001692.
93GB-00007673.
  93GB-00014384
  92GB-00015009
  (first entry)
20-SEP-1994 (first entry)
  Lewis I, Schneider H,
                                [Gly13] -hPTH (1-38) -OH.
  WPI; 1994-018352/03.
  (SANO ) SANDOZ LTD.
  Query Match
Best Local Similarity
Matches 23; Conserv
  Sequence 38 AA;
  18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APR-1993;
19-APR-1993;
  12-JUL-1993;
  15-JAN-1997
   WO9617942-A1
   13-JUN-1996.
  02-FEB-1994.
  GB2269176-A
  AAR98958;
  RESULT 12
ò
  g
  ÷
  The present invention provides a number of parathyroid hormone (PTH) or parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2 receptor agonists or antagonists and can be used in the treatment of disorders resulting from altered or excessive action of the PTH2 receptor, e.g. abnormal CNS functions, abnormal pancreatic functions, divergence from normal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or a hypothalmic disease. The present sequence is a peptide analogue of the invention
  New parathyroid hormone analogs, used for treating e.g. abnormal CNS or pancreatic functions, abnormal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or hypothalmic disease.
  Human; parathyroid hormone; parathyroid hormone-related protein; PTH; PTHFP; analogue; abnormal CNS function; pancreatic function; mineral metabolism; male infertility; abnormal blood pressure; hypothalmic dieses.
  Gaps
  ó,
  Match 61.7%; Score 100; DB 3; Length 34; Local Similarity 71.0%; Pred. No. 3.9e-05; es 22; Conservative 1; Mismatches 8; Indels
  'label= OTHER
'note= "OTHER=cyclohexylalanine"
  'note= "OTHER=cyclohexylalanine"
  1 SVSEIQXXHNXGKHLNSMERVEWLRKKLQDV 31
  'note= "C-terminal amide"
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV
  Human parathyroid hormone analogue #33.
  label= OTHER
note= "OTHER=des-Met"
  (SCRC ) SOC CONSEILS RECH & APPL SCI.
  Location/Qualifiers
  Rosenblatt M;
   AAR58104 standard; peptide; 38 AA.
  Claim 11; Page 39; 49pp; English.
  label= OTHER
  98US-00072956.
  99WO-US009521
                                    (first entry)
  Dong ZX,
  WPI; 2000-038790/03
  Sequence 34 AA;
  Key
Modified-site
  Modified-site
  Modified-site
  Modified-site
  Homo sapiens.
Synthetic.
  03-MAY-1999;
  05-MAY-1998;
                                    02-DEC-2002
  W09957139-A2
  11-NOV-11999.
  Chorev M,
  Query Match
Best Local S:
Matches 22,
    ABJ10737;
```

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Gaps

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95WO-US015800

07-DEC-1995;

AAR58104;

RESULT 11 AAR58104

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Sequence 84 AA;
   Sequence 84 AA;
   13-JUL-1990;
   13-JUL-1990;
  25-MAR-2003
22-JUN-1992
  WO9200753-A
  23-JAN-1992
   Synthetic.
   AAR23334;
  Query Match
   Matches
   AAR23334
   8
8×30000000×8
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  ö
   Regidues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M (M+ = cation), or -(C=O)NH2. 140 specific peptides derived from human PTH are given in the specification (AAR21150-256, AAR23226- 3250 + AAR23522-
  peptide employs a fusion protein construct (FPC) comprising a carbonic anhydrase and a variable fused polypeptide containing a target peptide. The method comprises precipitating either the FPC or a fragment of EPC including the carbonic anhydrase. An alternative method of producing the peptide comprises expressing the FPC as part of an inclusion body. The target peptides of the FPC are derived from growth hormone releasing factor (GRF), glucagon-like peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence corresponds to amino acids 1-38 of PTH
  New modified parathyroid hormone analogues - useful in treating cancer, osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
  De La Motte RS;
   Gaps
  Isolation and purificn of peptide(s) from fusion protein constructs which include a carbonic anhydrase and a variable fused polypeptide.
   method for the isolation and/or purification of a recombinant
  ö
  Length 38;
  Indels
  Manning SD,
   Pred. No. 4.4e-05;
1; Mismatches 7;
  Human parathyroid hormone analogue, [Gly6]hPTH.
   DB 2;
   SVSEIGLMHNLGKHLNSMERVEWLRKKLODV 31
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
   PTH; agonist; antagonist; receptor binding.
  61.7%; Score 100;
74.2%; Pred. No. 4
  Henriksen DB,
   3
   Strewler
   AAR21168 standard; protein; 84 AA
  Claim 15; Page 64; 86pp; English
   Claim 58; Page 50; 67pp; English.
   90US-00553760
  90US-00553760
           94US-00350530
   (revised)
(first entry)
   Local Similarity 74.2
nes 23; Conservative
  Nissenson RA,
  Stout JS,
Wagner FW;
  (REGC ) UNIV CALIFORNIA
                                (BION-) BIONEBRASKA INC
  WPI; 1992-056643/07.
   WPI; 1996-287186/29
   Sequence 38 AA;
   Partridge BE,
Holmquist B,
           07-DEC-1994;
   13-JUL-1990;
   13-JUL-1990;
  25-MAR-2003
17-JUN-1992
   WO9200753-A
  23-JAN-1992
   Synthetic.
  Cohen FA,
  Query Match
  Matches
  AAR21168
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  Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M (M+ = cation), or -(C=O)NH2. 142 specific peptides derived from bovine PTH are given in the specification (AAR23251-382, and AAR23540-549). Corresp. peptides created using residues 7-84 of human and porcine PTH are also claimed. All have mutations at positions 3, and/or 6, and/or 9 which result in surface side chains which are useful to modulate receptor binding and activity. They are useful as agoniets and antagonists in the treatment of condi-tions or diseases involving PTH. The peptides are pref. prepd. by solid phase synthesis. See also AAR21257 (human generic), AAR21258 (bovine generic) and AAR21259 (porcine generic). (Updated on 25-MAR-2003 to correct PA field.)
  ö
PTH are also claimed. All have mutations at positions 3, and/or 6, and/or 9 which result in surface side chains which are useful to modulate receptor binding and activity. They are useful as agonists and antagonists in the treatment of condi- tions or diseases involving PTH. The poptides are pref. prepd. by solid phase synthesis. See also AAR21257 (human generic), AAR21258 (bovine generic) and AAR21259 (porcine
   New modified parathyroid hormone analogues - useful in treating cancer, osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
   Gaps
  Gaps
   ö
  .
0
   Length 84;
   Indels
  Indels
   Length
  Score 99; DB 2; Le.
Pred. No. 0.00013;
1; Mismatches 7;
  Score 100; DB 2; L
Pred. No. 9.6e-05;
1; Mismatches 7;
  Bovine parathyroid hormone analogue, [Gly6]bPTH.
  SVSEIGLMHNLGKHLNSMERVEWLRKKKLQDV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  PTH; agonist; antagonist; receptor binding.
   Strewler GJ;
   AAR23334 standard; protein; 84 AA
  Claim 15; Page 64; 86pp; English.
  61.1%;
74.2%;
   61.7%;
74.2%;
   90US-00553760
  90US-00553760
   (first entry)
   Query Match
Best Local Similarity 74.2
Matches 23; Conservative
  Local Similarity 74.2
nes 23; Conservative
   Cohen FA, Nissenson RA,
   (REGC ) UNIV CALIFORNIA
  (revised)
  WPI; 1992-056643/07.
```

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The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is cyclohexylalanine (Cha). In this example the Leu residue at position 7 and the Leu at position 11 in the wild-type have been substituted by Cha. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin). N.B. The present sequence does not appear in the modification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim
   New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture.
   Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
   Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
   Query Match 60.5%; Score 98; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 6.9e-05; Matches 22; Conservative 1; Mismatches 8; Indels
   /label= OTHER
/note= "Cyclohexylalanine (Cha)"
1 AVSEIGFMHNLGKHLSSMERVEWLRKKLQDV 31
  /note= "In amide form"
   Location/Qualifiers
  AAW17939 standard; peptide; 34 AA
   95US-0001105P.
95US-0003305P.
96US-00626186.
   /label= OTHER
/note= "Cha"
  Claim 5; Page; 33pp; English.
  96WO-US011292.
   29-JUL-1997 (first entry)
   (BIOM-) BIOMEASURE INC.
   WPI; 1997-118819/11.
  Sequence 34 AA;
   Key
Modified-site
  13-JUL-1995;
06-SEP-1995;
29-MAR-1996;
  Modified-site
   Modified-site
  Homo sapiens.
Synthetic.
  03-JUL-1996;
   WO9702834-A1
   30-JAN-1997.
   AAW17939;
   Dong ZX;
  RESULT 15
AAM17939
AAM17939
AXX
AAW17939
XXX
AAW17
AAW17
XXX
AAW17
A
                                    g
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Gaps .; 0

> > q

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Search completed: November 21, 2005, 16:10:12 Job time : 142.5 secs
```

Н

sw model - protein search, using OM protein November 21, 2005, 16:05:13; Search time 23.5 Seconds Run on:

(without alignments) 126.924 Million cell updates/sec

US-09-475-158A-5 162 1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV Perfect score: Sequence:

31

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* \*:08 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|       | Description | parathyroid hormon | ABC transport prot | related to proline | transcription fact | early growth respo | myc far upstream e | probable DNA bindi | regulatory protein | probable protein p | neurogenic locus m | 1-phosphatidylinos | endo-1,4-beta-xyla | hypothetical prote | hypothetical prote | hypothetical prote | AcrB/AcrD/AcrF fam |        | hypothetical prote |        | acp-22 protein - y | hypothetical prote | protein F17L21.18 | ein trihel | hdc protein - frui | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|       | ID          | PTHU               | PTBO               | JC4202             | PTPG               | A05091             | 151851             | T18288             | T49559             | S71795             | A41211             | A53184             | T03605             | A41696             | T13926             | A33106             | T18273             | 140712             | T45737             | 669963             | D96664             | G87398             | G84746 | T49450             | S16063 | S32224             | T49792             | D86399            | B86456     | S58064             |
|       | DB          | -                  | Н                  | ~                  | <del>, -</del>     | ~                  | ~                  | 7                  | ~                  | 7                  | N                  | ~                  | ~                  | ~                  | ~                  | 7                  | ~                  | -                  | ~                  | 7                  | ~                  |                    | ~      |                    |        |                    |                    |                   | ~          | 7                  |
|       | Length DB   | 115                | 115                | 115                | 115                | 115                | 105                | 1336               | 212                | 440                | 543                | 644                | 425                | 1090               | 1428               | 1596               | 1858               | 644                | 252                | 486                | 415                | 1047               | 1066   | 199                | 199    | 199                | 201                | 209               | 594        | 649                |
| ,     | ~-          | 56.8               | 56.2               | 54.3               | 51.9               | 47.5               | 44.4               | 40.7               | 39.5               | 39.5               | 39.5               | 39.2               | 38.9               | 38.9               |                    | 38.9               | 38.9               | 38.6               | 38.3               | 38.3               | 38.0               | 38.0               | 38.0   | 37.7               | 37.7   | 37.7               | 37.7               | 37.7              | 37.7       | 37.7               |
| Č     |             | 1                  |                    | _                  |                    | _                  | •                  |                    | _                  | _                  | _                  |                    | _                  | _                  | _                  | _                  | _                  |                    |                    | 7                  |                    |                    |        | _                  | _      | _                  |                    |                   | _          | _                  |
|       | Score       | 95                 | 9                  | 88                 | 8                  | 7.7                | 72                 | 99                 | 9                  | 9                  | 9                  | 63.5               | 9                  | 9                  | 9                  | 9                  | 9                  | 62.5               | 9                  | <b>3</b> 6         | 61.                | 61.5               | 61.5   | 6                  | 9      | 9                  | 61                 | 9                 | 9          | 9                  |
| 1,000 | No.         | 1                  | 7                  | e                  | 4                  | ស                  | 9                  | 7                  | 80                 | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 50                 | 21                 | 22     | 23                 | 24     | 25                 | 56                 | 27                | 28         | 29                 |

| 671 2 A35912<br>239 2 S49193<br>315 2 T41868<br>316 2 T06612<br>500 2 T20961<br>250 2 T20961<br>251 2 F84596<br>261 2 A46179<br>267 2 A60643<br>396 2 T49109<br>443 1 S29334<br>445 1 S31224 | homeotic protein o | probable deoxyribo | GCR 101 protein - | hypothetical prote | glycine-rich prote | neurotrophin-4 pre | U2 BNRNP auxiliary | antigen 5401 - Eim | glycine-rich prote | UL44 protein - hum | transcription fact | transcription fact | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|                                                                                                                                                                                              | A35912             | S57795             | 849193            | T41868             | T06612             | T20961             | T27407             | B86427             | F84596             | A42687             | A46179             | A60643             | T49109             | QQBEV2             | S29334             | S31224             |
|                                                                                                                                                                                              | 2                  | 7 2                | 9                 | 5                  | 9                  | 0                  | 0                  | 2                  | 1 2                | 0                  | 0                  | 7 2                | 9                  | 3 1                | 3                  | 2                  |
|                                                                                                                                                                                              | 37.7               | 37.7               | 37.0              | 37.0               | 37.0               | 37.0               | 37.0               | 36.7               | 36.4               | 36.4               | 36.4               | 36.4               | 36.4               | 36.4               | 36.4               | 36.4               |
| U                                                                                                                                                                                            | 61                 | 61                 | 09                | 9                  | 9                  | 9                  | 09                 | 59.5               | 29                 | 59                 | 59                 | 29                 | 59                 | 29                 | 59                 | 59                 |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                        | 30                 | 31                 | 32                | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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parathyroid hormone precursor [validated] - human
NyAlternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004
C;Accession: A19339; S53790; A33169; A33189; A93783; A93783; A90387; A90456; A94410; I38
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McJevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McJevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McJevitt, B.E.; Preeman, M.W.; Pennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McJevitt, B.E.; Preeman, M.W.; Pennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Reference number: A19339; MUID:83169834; PMID:6220408

A;Molecule type: DNA A;Residues: 1.115 «VAS. A;Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:g190702; PIDN R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K. Biol. Chem. Hoppe-Seyler 375, 821-824, 1994 A;Title: Purification of meprin from human kidney and its role in parathyroid hormone d∈ A;Reference number: S53790; MUID:95225988; PMID:7710697

A; Accession: S53790

A; Molecule type: protein
A;Reaidues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Reaidues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3
A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurr
R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A;Title: Structural analysis of human proparathyroid hormone by a new microsequencing a;
A;Reference number: A93169; MUID:74174967; PMID:4833516

A;Accession: A93169 A;Molecule type: protein A;Residues: 26-37 <JAC.> A;Cross-Acences: UNIPARC:UPI00001734E4 A;Cross-Acences: UNIPARC:UPI00001734E4 R;Olstead, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.: Eur. J. Biochem. 205, 311-319, 1992

A, Title: Isolation and characterization of two biologically active O-glycosylated forms

A; Reference number: S21199; MUID:92209518; PMID:1555591 A; Accession: S21199

A; Molecule type: protein
A; Residues: 32-114, N° <0LS>
A; Residues: 32-114, N° <0LS>
A; Residues: 32-114, N° <0LS>
A; Cross-references: UNIPARC.UPI00001734ES
A; Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation
B; Niall, H.D.; Sauer, R.T.; Jacoba, J.W.; Keutmann, H.T.; Segre, G.V.; O'Rlordan, J.L.H
Proc. Natl. Acad. Sci. US.A. 71, 384-388, 1974
A; Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid
A; Reference number: A93789; MUID:74111656; PMID:4521809

A; Accession: A93789

A;Molecule type: protein
A;Residues: 32-68 «NIA»
A;Residues: 32-68 «NIA»
A;Cross-references: UNIPARC:UP1000002DA05
R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D. Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

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  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WED.
A;Crosidues: 1-115 <WED.
B;Residues: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID
R;Weaver, C.A.; Gordon, D.F.
  Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA
                       31
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV
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A,Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues 1 A,Foceania (A)75 and A,Fo
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Cisuperfamily: parathytoid hormone, parathyroid gland; hormone homology
Cisuperfamily: parathytoid djand; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-31/Domain: propeptide #status experimental <PRO>F;30-64/Domain: parathyroid hormone homology <PTH>F;30-64/Domain: parathyroid hormone #status experimental <PMAT>F;32-115/Product: parathyroid hormone #status experimental <PMAT>
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A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino A;Reference number: A90390; MUID:76018954; PMID:1164500 A;Accession: A90390
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A; Residues: 26-115 < CHU>
A; Residues: 26-115 < CHU>
A; Cross-references: UNIPARC: UP100001592DF
B; Cross-references: UNI H.D.; Hegan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J
Biochemistry 13, 1994-1999, 1974
A; Title: The amino acid sequence of porcine parathyroid hormone.
A; Reference number: A90376; MUID: 74253317; PMID: 4840833
   A;Cross-references: UNIPARC:UP100001734E0
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormor
A;Reference number: A90030; MUID:74173303; PMID:4598526
  A; Contents: annotation

(S. Superfamily: parathyroid hormone, parathyroid diand)

(S. Superfamily: parathyroid parathyroid gland

(S. Superfamily: parathyroid berance #status predicted (SIG)

(P. 1-25/Domain: signal sequence #status predicted (SIG)

(P. 100main: propeptide #status experimental (PRO)

(P. 30-64/Domain: parathyroid hormone homology (PTH)

(P. 32-115/Product: parathyroid hormone #status experimental (MAT)
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64.5%; Pred. No. 0.0041;
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  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
   3; Mismatches
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   47.5%;
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Matches 20; Conservative
  Best Local Similarity 61.3
Matches 19; Conservative
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  A; Residues: 1-115 <SCH>
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   A; Accession: A90376
   A; Accession: A05091
   A; Introns: 29/3
C; Superfamily: F; 30-64/Domain:
  32
  Query Match
   Query Match
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Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: 145976; MUID:83105964; PMID:6185374
A;Accession: 145976
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: PTH
A;Introns: 29/2
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C;Keywords: hormone: parathyroid hormone #status experimental <PWAT>
F;26-115/Ponduct: propertide #status experimental <PRO>F;30-64/Domain: parathyroid hormone homology or PRO>F;30-64/Domain: parathyroid hormone homology or PRO>F;30-64/Domain: parathyroid hormone homology or PRO>F;30-64/Domain: parathyroid hormone momely or PRO>F;31-115/Product: parathyroid hormone #status experimental <PMAT>
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C; Species: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C; Species: Lo. Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C; Accession: JC4202
R; Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A; Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and
A; Reference number: JC4202
A; Molecule type: mRNA
A; Resession: JC4202
A; Molecule type: mRNA
A; Residues: L-115 <ROS>
A; Rocession: JLS <ROS>
A; Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:G558915; PIDN:
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C; Keywords: hormone
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F; 30-64/Domain: parathyroid hormone homology <PTH>
F; 32-115/Product: parathyroid hormone #status predicted <MAT>
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Cispecies: Sus serofa domestica didomestic pig)
Cispecies: Sus serofa domestica (domestic pig)
Cispecies: Sus serofa domestica (domestic pig)
Cistes: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
Ciscomelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A; Reference number: A26806; MUID: 87316938; PMID: 3628009
A; Reference number: A26806; MUID: 87316938; PMID: 3628009
A; Reference number: A26806; MUID: 87316938; PMID: 3628009
A; Residues not compared with conceptual translation
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A; Cross-references: UNIPROT: PO1269; UNIPARC: UPI000013290B; GB: X05722; GB: X00409; NID: G18
R; Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
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   ch 54.3%; Score 88; DB 2; Length 115; 1 Similarity 67.7%; Pred. No. 0.0014; 21; Conservative 2; Mismatches 8; Indels
   Length 115;
  Indels
   Query Match 56.2%; Score 91; DB 1; Lei
Best Local Similarity 71.0%; Pred. No. 0.00062;
Matches 22; Conservative 1; Mismatches 8;
  32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62
   32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  Best Local Similarity
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Length 115;

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A; Residues: 1-115 < HBI>
A; CRESidues: 1-115 < HBI>
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A; CRESIN < HBI
CRESIDER: CRESI
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   parathyroid hormone precureor - rat
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05091; A26080
R;Heinrich, G:; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
A;Reference number: A05091; MUID:84135846; PMID:6321505
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8; Indels
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Pred. No. 0.028;
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  Jarshy Parathyroid hormone - rat (fragment)
parathyroid hormone - rat (fragment)
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 151851
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleocitde sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Arcession: 151851
A;Accession: 105 AERS
A;Cross-references: UNIPARC:UP1000170AE0; GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:C;Genetics:
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NAlternate names: protein B208.70
Cispecies: Neurospora crassa
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  9; Indels
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   6 GGGGGGGLNSMERVE 22
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A,Title: nit-4, a pathway-specific regulatory gene of Neurospora crassa, encodes a prote
A,Reference number: A41696, MUID:92017855, PMID:1840634
A,Accession: A41696
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NyAlternate names: mastermind protein
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: A36391; A33106; E13514
R;Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
R;Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
A;Title: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually
A;Reference number: A36391
A;Accession: A36391
  C)Accession: T13926
R;Dick, T.; Bahri, S.M.; Chia, W.
R;Dick, T.; Bahri, S.M.; Chia, W.
A;Dick, T.; Bahri, S.M.; Chia, W.
A;Title: Drosophila DPP2C1, a novel member of the protein phosphatase 2C (PP2C) family.
A;Reference number: Z17810; MUID:98019081; PMID:9358049
A;Accession: T13926
   A; Molecule type: DNA
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A; Residues: 1-1090 < YUD.>
A; Cross-references: UNIPROT: P28349; UNIPARC: UPI00001301D7; GB: M80368
A; Yuan, G.F.; Fu, Y.H.; Marzluf, G.A.
submitted to the EMBL Data Library, December 1991
A; Description: nit-4, a pathway-specific regulatory gene of Neurospora crassa, encodes
A; Reference number: $37629
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   probable protein phospharase 2C1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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  A,Introns: 529/2
C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger
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  Cyactes: Annual Toy Mateuda, T.; Adachi, T. Balant M.; Aoki, N.; Mateuda, T.; Adachi, T. Balant Mol. Biol. 33, 513-522, 1997
A;Title: Characterization of a novel rice bZIP protein which binds to the alpha-globulin A;Reference number: Z14974; MUID:97201485; PMID:9049271
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C;Accession: A53184
R;Duncan, R; Bazar, L; Michelotti, G; Tomonaga, T; Krutzsch, H; Avigan, M; Levens, Genes Dev. 8, 465-480, 1994
A;Itle: A sequence-specific, single-strand binding protein activates the far upstream ep. 74. A; Accession: A53184
A; Accession: A53184
A; MulD: 94170991; PMID: 8125259
A; Accession: A53184
A; MulD: 944 cDUN
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K;Yuan, G.F.; Fu, Y.H.; Marzlut, G.A.
Mol. Cell. Biol. 11, 5735-5745, 1991
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
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macaca fasc
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## ALIGNMENTS

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MEDLINE=82150870; Wabde=6950381;
MEDLINES-82150870; WARM. Potts J.T. Jr., Rich A.;
"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
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MEDLINE=83169834; PubMed=6220408;
Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N.,
Potts J.T. Jr., Rich A., Kronenberg H.M.;
"Nucleotide sequence of the human parathyroid hormone gene.";
Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
   PROTEIN SEQUENCE OF 32-68.

MEDLINE=1411656; PubMed=4521809;
Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
Niall H.D., Sauer R.T., Pachs J.T., Notte J.T. Jr.,

"The amino-acid sequence of the amino-terminal 37 residues of human
   Jr.;
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Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
   Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. «
"Structural analysis of human proparathyroid hormone by a new
  [6]
PROTEIN SEQUENCE OF 61-83 AND 84-115.
MEDLINE=79082855; PubMed=728431;
Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
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   Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974)
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Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T., in Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.";

Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
  MEDIATE-9199748; PubMed=2069952; MEDIATE-9199748; PubMed=2069952; Mayer B., Wingender E., Mayer H.; Klaus W., Dieckman T., Waray V., Schomburg D., Wingender E., Mayer H.; Investigation of the solution structure of the human parathyroid hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and molecular dynamics calculations."; Biochemistry 30:6936-6942(1991).
  STRUCTURE BY NMR OF 32-70.

MEDILINE-20090619; PubMed410623601; DOI=10.1006/bbrc.1999.1958;

MARY U.C., Adermann K., Bayer P., Foresmann W.-G., Rosch P.;

"Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";

Blochem. Blophys. Res. Commun. 267:213-220(1000).
  SEQUENCE REVISION.
MEDINE-73146516; PubMed=1125201;
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KEULMEADN H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
"A reinvestigation of the amino-terminal sequence of human parathyroid"
   STRUCTURE BY NMR OF 32-68.
MEDILINE=595180B04; PubMed=797503; DOI=10.1074/jbc.270.25.15194;
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Keutemann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N., O'Riordan J.L.H., Potts J.T. Jr.;
O'Riordan J.L.H., Potts J.T. Jr.;
CIN] Talmadge R.V., Owen M., Parsons J.A. (eds.);
Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).
  STRUCTURE BY NMR OF 32-65.
MEDDIJNE=93345518; PubMed=8344299;
Barden J.A. Cuthbertson R.M.;
"Stabilized NMR structure of human parathyroid hormone(1-34).";
Eur. J. Biochem. 215:315-321(1993).
             of human parathyroid hormone.";
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MEDLINE=91009811; PubMed=2212001;
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Kronenberg H.M.;
"Mutation of the signal peptide-encoding region of the preproparathyroid hormone gene in familial isolated
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Madbline=7327467; PubMed=4721748;
Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
Riniker B., Rittel W., Sieber P.;
Synthesis of sequence 1-34 of human parathyroid hormone.";
Helv. Chim. Acca 56:470-473(1973).
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J. Clin. Invest. 86:1084-1087(1990)
  "A reinvestigation of the amino-chormone.";
Biochemistry 14:1842-1847(1975).
 Potts J.T. Jr.;
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   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was as long as its content is in no way modified and this statement is not removed
Sunthornthepvarakul T., Churesigaew S., Ngowngarmratana S.;
"A novel mutation of the signal peptide of the preproparathyroid
hornone gene associated with autosomal recessive familial isolated
hypoparathyroidism."
J. Glin. Endocrinol. Metab. 84.3792-3796 (1999)
Doc and preventing their renal excretion.
I. PUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
I. SUBCELLULAR LOCATION: Secreted.
I. DISEABS: Defects in PTH are a cause of familial isolated
hypoparathyroidism (FIH) [MIM.146200]. FIH exist both as autosomal
dominant and recessive forms of hypoparathyroidism.
I. SIMILARITY: Belongs to the parathyroid hormone family.
  Parathyroid hormone.

C -> R (in FIH; dominant; leads to inefficient processing of the precursor).

FridavAR 006047.

S -> P (in FIH; recessive, might lead to inefficient processing of the precursor).

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   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Intaliand.";
J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
I. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
I. FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
I. SUBCELLULAR LOCATION: Secreted.
I. SUBCELLULAR LOCATION: Secreted.
I. SIMILARITY: Belongs to the parathyroid hormone family.
  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
   ..
                            ö
  Ouery Match 56.8%; Score 92; DB 1; Length 115; Best Local Similarity 71.0%; Pred. No. 0.0031; Matches 22; Conservative 1; Mismatches 8; Indels
                            Indels
  1 25 By similarity.
26 31 By similarity.
32 115 Parathyroid hormone.
115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;
   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyroid hormone, preproprotein.
                            ..
   16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
  0.0031;
  115 AA
   32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62
  115 AA
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  32 SVSEIQLMHNLGKHLNSMERVEWLRKKLODV 62
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
HSSP; P01270; 1ET1.
       Pred. No. 0.00
1; Mismatches
  Cercopithecidae; Cercopithecinae; Macaca.
   InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001415; Parbyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub; 1.
Pfam; PP01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
SNART; SM00087; Pthyrhorm_sub; 1.
SNART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
  PRT;
   16-OCT-2001 (Rel. 40, Created)
71.0%;
  Q4VB48 HUMAN PRELIMINARY;
Q4VB48;
                          22; Conservative
  STANDARD;
       Similarity
   Hormone; Signal.
   NCBI_TaxID=9541;
  MACFA
  SEQUENCE
   HUMAN
  removed
       Best Local
   PROPEP
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Gaps

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RESULT 3 Q4VB4B HU ID Q4VB AC Q4VB DT 13-S DT 13-S DT 13-S DE Para GN Name

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Length 115; Indels

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   [9]

STRUCTURE BY NMR OF 32-68.

MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=200619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=2009099; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=2009099; PubMed=10623601; DOI=10623601;

MEDLINE=2009099
  [5]
PROTEIN SEQUENCE OF 26-115.
MEDLINE-74142666; PubMed=4522780;
Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
Cohn D.V.,
"The N-terminal amino-acid sequence of bovine proparathyroid
Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A., Potts J.T. Jr., Rich A.;
Cloning and nuclectide sequence of DNA coding for bovine preproparathyroid hormons.";
Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
  SYNTHESIS OF 32-65.

SYNTHESIS OF 32-65.

MEDLINE=71.091588; PubMed=4322265;

MEDLINE=71.091588; PubMed=4322265;

MEDLINE=71.091588; PubMed=4322265;

MEDLINE=71.091 H.D., Sauer R.,

Deffeos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;

"Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyroid hormone.";

Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
   MEDLINE-82037785; PubMed-6170060; Meaver C.A., Gordon D.F., Kemper B.; Maraver C.A., Gordon D.F., Kemper B.; Mintroduction by molecular cloning of artifactual inverted sequences at the 5' terminus of the sense strand of bovine parathyroid hormone
   NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207 (82)90136-8;
Weaver C.A., Gordon D.F., Kemper B.;
Waver C.A., Gordon D.F., Kemper B.;
Waver C.A., Gordon D.F., Kemper B.;
Waver C.B., Gordon D.F., Selection C. 28:411-424(1982).
  [4]
MEDLINE-8426483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
"Isolation and complete nucleotide sequence of the gene for bovine
   PROTEIN SEQUENCE OF 32-115.

MEDLINE=71076162, Pubmed=5531031;

Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,

Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,

Authach G.D., Potts J.T. Jr.,

"The amino acid sequence of bovine parathyroid hormone I.";

Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).

PROTEIN SEQUENCE OF 32-115.

MEDLINE=71063634; Pubmed=5275384;

Brewer H.B. Jr., Roman R.,

"Bovine parathyroid hormone: amino acid sequence.";

Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981)
  Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974)
  parathyroid hormone.";
Gene 28:319-329(1984).
   (2)
NUCLEOTIDE SEQUENCE.
   CDNA."
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Gaps
   wholevoline beducand A.R., Lyons L.A., O'Brien S.J., Laughlin T.F., Murray J.D., Bowling A.T.; Edetand A.T.; Caetand A.T.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF13423; AAF62347.1; -; Genomic_DNA.

EMBL; AF13423; AAF62347.1; -; Genomic_DNA.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005179; F:hormone activity; IEA.

InterPro; IPR001415; Parathyrd_hrm.

InterPro; IPR001411; Phythorm_sub.

PANTHER; PFHRIOS41; Phythorm_sub; 1.

Pfam; PF01279; Parathyrdorm_sub; 1.

Pfam; PF01279; Parathyrdorm_sub; 1.
   Name-Erus
Eguus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
   NUCLECTIDE SEQUENCE.
MEDILINE-200829-17: PubMed=10613847; DOI=10.1101/gr.9.12.1239;
MEDILINE-200829-17: PubMed=10613847; DOI=10.1101/gr.9.12.1239;
Cacteano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1249(1999).
  ö
EMBL; V00106; CAA23439.1; -; mRNA.
EMBL; V00106; CAA23747.1; -; mRNA.
EMBL; MC1038; AAA30749.1; -; mRNA.
EMBL; MC1038; AAA30749.1; -; Genomic_DNA.
EMBL; MC1038; AAA30749.1; -; mRNA.
EMBL; MC2082; AAA30748.1; -; mRNA.
PIR, 12WC; NRR; G=32-68.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001355; Parathyrdorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
PRODOM; PRO10379; Parathyroid; 1.
ProDom; PR01083; PTH; 1.
ProDom; PR01083; PTH; 1.
PROSTIE; PR01083; PTH; 1.
PROSTIE; PR00135; PRATHYROID; 1.
PROSTIE; PR00335; PARATHYROID; 1.
PROSTIE; PS00335; PARATHYROID; 1.
ID structure; Direct protein sequencing; Hormone; Signal.
SIGNAL.
   56.2%; Score 91; DB 1; Length 115; 71.0%; Pred. No. 0.0041; cive 1; Mismatches 8; Indels
   115 Parathyroid hormone.

106 V -> G (in Ref. 4).

40

42

52

52

60

63

1, 12980 MW; ZED246B348880710 CRC64;
   9805 MW; 253184EA681A2022 CRC64;
  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TUN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone (Fragment).
  86 AA.
  32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  PRT;
  PROSITE; PS00335; PARATHYROID; 1.
   Query Match
Best Local Similarity '--
Local Similarity '--
22; Conservative
  Q9N1VO_HORSE PRELIMINARY;
   NUCLEOTIDE SEQUENCE.
   26
32
106
37
41
51
51
115 AA;
  NCBI_TaxID=9796;
  SM00087
  NON TER
SEQUENCE
   CHAIN
CONFLICT
HELIX
   SEQUENCE
   5
HORSE
   PROPEP
  09N1V0
   CONTROLL CON
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115 AA.

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PROTEIN SEQUENCE OF 32-115.

MEDLINE-4253317; PubMed-4840833;
Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
Potts J.T. Jr.,
"The amino acid sequence of porcine parathyroid hormone.";
"The Biochemistry 13:1994-199911974).
-i- FUNCTION: PTH elevates calcium level by dissolving the salts in
  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
  MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
Porcine proparathyroid hormone. Identification, biosynthesis, and
partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
   MEDLINE=87316938; PubMed=3628009; Schmelzer H.-J., Gross G., Widera G., Mayer H.; Schmelzer H.-J., Gross G., Widera G., Mayer H.; Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
                        21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH)
   PROTEIN SEQUENCE OF 26-115
STANDARD;
   Mammalia; Eutheria;
   NUCLEOTIDE SEQUENCE
   NCBI_TaxID=9823;
  Sus scrofa (Pig)
  SEQUENCE
   Query Match
   removed.
               901269;
  PROPEP
   SIGNAL
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   Gaps
  Gaps
  Capen C.C.; "Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone."; Gene 160:241-243(1995).
   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
  MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
   Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.
   -:- FUNCTION: FTH elevates calcium level by dissolving the salts bone and preventing their renal excretion.
-:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: Belongs to the parathyroid hormone family.
   ö
  ö
  54.3%; Score 88; DB 1; Length 115; 67.7%; Pred. No. 0.0093;
             Query Match
Best Local Similarity 67.7%; Pred. No. 0.0069;
Matches 21; Conservative 2; Mismatches 8; Indels
   Indels
   25 By similarity.
31 By similarity.
115 Parathyroid hormone.
12957 MW; FC38F77F1C8CFE56 CRC64;
  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
  Ensembl; ENSCAFGO000008177; Canis familiaris.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001825; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
   32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62
  115 AA
   1 AVSEIGGGGGGGGGLNSMERVEWLRKKLODV 31
   2; Mismatches
   EMBL; U15662; AAA82584.1; -; mRNA.
PIR; JC4202; JC4202.
  Conservative
   STANDARD;
   Canis familiaris (Dog)
  NUCLEOTIDE SEQUENCE.
TISSUE=Parathyroid;
  32 1
115 AA;
  HSSP; P01268; 1ZWC
  Similarity
   Canis.
NCBI_TaxID=9615;
   Hormone; Signal
   21;
  CANFA
  SEQUENCE
   Name=PTH:
  Query Match
  removed.
  Local
  SIGNAL
   PTHY CANFA
  PTHY
  Matches
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   Gaps
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bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
  Length 115;
  115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;
  Parathyroid hormone
  Score 84; DB 1;
Pred. No. 0.028;
3; Mismatches
   Ą.
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   62
   Direct protein sequencing; Hormone; Signal.
   115
   32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDV
   HSSP; PO1270; 1BWX.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_gub.
PANTHER; PTHR10541; Pthyrhorm_gub;
Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
   Pthyrhorm_sub; 1.
   PRT;
   EMBL; X05722; CAA29193.1; -; mRNA.
PIR; B26806; PTPG.
  PROSITE; PS00335; PARATHYROID; 1.
  51.9%;
64.5%;
  20; Conservative
   STANDARD;
   115
   ProDom; PD010687; Pthy
SMART; SM00087; PTH;
  Local Similarity
   PTHY_FELCA
ID _PTHY_FELCA
   RESULT 8
```

PTHY\_PIG RESULT 7

```
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Amrinae, Rattus.
  Gaps
   TISSUE=Parathyroid;
Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
  salts in
  rat
  NUCLEOTIDE SEQUENCE OF 32-115.
STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
MEDLINE=56679910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
  NUCLEOTIDE SEQUENCE.
MEDINE-84135846; PubMed=6321505;
MEDINE-84135846; PubMed=6321505;
MEDINE-67135846; PubMed=6321505;
MEDEN G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
"Gene encoding parathyroid hormone. Nucleotide sequence of the gene and deduced amino acid sequence of rat preproparathyroid hormone."
   47.5%; Score 77; DB 2; Length 105; 61.3%; Pred. No. 0.17; 1ve 3; Mismatches 9; Indels
  NUCLECTIDE SEQUENCE.

MEDILINE=87316938, PubMed=3628009;
Schmelzer H.-J., Gross G., Widera G., Mayer H.:

"Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
Endocrinology 136:5600-5607(1995).

R HSSP, 80127; AAP23220.1; -; mRNA.

R HSSP, P01270; 12MB.

R GQ:0005776; C:extracellular region; IEA.

R InterPro: IPR001415; Parathyrd_hrm.

R InterPro: IPR001415; Parathyrd_hrm.

R InterPro: IPR003625; Pthyrhorm_sub.

R PANTHER; PFHR10541; Pthyrhorm_sub; 1.

R PRSP; PRSP001832; PTH; 1.

R PRODOM; PD010697; Pthyrhorm_sub; 1.

R PRODOM; SMO087; Pthyrhorm_sub; 1.

R SMART; SMO087; PTH; 1.

R PROSTIF; PR00335; PARATHYROID; 1.
   THY RAT STANDARD; PRT; 115 AA.

1D PTHY RAT STANDARD; PRT; 115 AA.

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Parathyroid hormone precursor (Parathyrin) (PTH).
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  22 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 52
   Gene Technol. 21:228-229(1984).
  Biol. Chem. 259:3320-3329(1984).
   NUCLEOTIDE SEQUENCE OF 10-115.
  Query Match
Best Local Similarity 61.3%;
Marches 19; Conservative
   NCBI_TaxID=10116;
   hormone.";
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  Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
  Gaps
  (1)—

**COLECTIDE SEQUENCE.**

**NOTION OF REAL MODE OF THE PREPARED TO C.C., ROSOL T.J.;

**NOTION OF REAL MODE OF THE PREPARED TO COLED OF THE OF T
  Felis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Pelinae, Felis.
  STRAIN=Sprague-Dawley;
MEDILINE=56079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
  ;
0
   Query Match 50.0%; Score 81; DB 1; Length 115; Best Local Similarity 61.3%; Pred. No. 0.063; Matches 19; Conservative 4; Mismatches 8; Indels
  By similarity.
By similarity.
Parathyroid hormone.
80CD557CC6AlA47E CRC64;
  Last sequence update)
Last annotation update)
            05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathbyroid hormone precursor (Parathyrin) (PTH).
   105 AA.
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  INCESTRON LAW.

INCESTRON PRODUCTS, PRACHLYND ARM.
INCESTRON IPRODUCTS SE PLYNYCHOR SUD.
PANYHER, PTHRIOS41, PCHYNYCHOR SUD, PERSPOOLS54, PRESPOOLS32, PTH, 1.
PRODUM, PD010687, PCHY, 1.
PRODUM, PD010687, PCHY, 1.
PROSITE, PS00335, PRARTHYROID, 1.
   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Hypothalamic parathyroid hormone.
Name=PTH-(1-84);
  EMBL; AF309967; AAG30545.1; -; mRNA.
HSSP; P01268; 1ZWC.
   PRT;
  1 25 By
26 31 By
32 115 Pe
115 AA; 12921 MW;
  Q80WZ2_RAT PRELIMINARY;
  NUCLEOTIDE SEQUENCE.
  SEQUENCE
  removed.
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  Eukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
   Gaps
   Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.; "Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
  TISSUE=Thyroid;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
   ö
   Score 77; DB 1; Length 115;
Pred. No. 0.19;
   Indels
  C -> Y (in Ref. 3).
A -> T (in Ref. 3).
A -> I (in Ref. 3).
V -> G (in Ref. 3).
7B434CFCA528B230 CRC64;
   01-MAY-1999 (TrEMBLrel. 10, Created)
(1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyroid hormone precursor.
   6
  ENSRNOG00000014318; Rattus norvegicus.
   115 AA
  32 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 62
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   Pred. No. 0.19
3; Mismatches
   EMBL; K01268; AAA41979.1; -; Genomic_DNA.
EMBL; X05721; CAA29192.1; -; mRNA.
EMBL; M54875; AAA57156.1; -; mRNA.
   EMBL; S80127; -; NOT_ANNOTATED_CDS; mRNA.
PIR; A05091; A05091.
  Parathyroid
  RGD; 3440; Pth.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR003626; PTH related.
InterPro; IPR003625; Pthyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub; Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
   PRT;
   ProDom; PD013225; PTH related; 1.
ProDom; PD010687; Pthyrhorm sub; 1.
   SMART; SM00087; PTH; î.
PROSITE; PS00335; PARATHYROID; 1.
   25
31
115 Pa
18 C
23 A
33 V
62 V
12722 MW;
  >>
   Query Match
Best Local Similarity 61.3%;
Matches 19; Conservative
   Q9Z0L6_MOUSE PRELIMINARY;
Q9Z0L6;
  Mus musculus (Mouse)
   [1]
NUCLEOTIDE SEQUENCE.
  [2]
NUCLEOTIDE SEQUENCE.
  32
18
23
33
62
115 AA;
   HSSP; P01270; 1ZWB.
  NCBI_TaxID=10090;
   Hormone, Signal
   STRAIN=129/Sv;
  Name=Pth;
  CONFLICT
CONFLICT
CONFLICT
SEQUENCE
  CHAIN
  Ensemb1;
  removed.
  MOUSE
  SIGNAL
   EMBL;
EMBL;
  RESULT 11
  ACOUNTY OF THE PART OF THE PAR
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Maria M.A., Schein J.E., Jones S.J.M., Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.; and mouse CDNA sequences ".
   Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
  Gaps
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0
  MXII MOUSE STANDARD; PRT; 1493 AA.
P53349; Q60831; Q9R0U3; Q9R256;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitogen-activated protein kinase kinase last annotation was kinase last sequence was kinase la (MEK kinase la (MEK la (MOUSE)).

Mus musculus (Mouse).
   NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC09456.1; -; Genomic_DNA.
EMBL; AC009456.1; -; MRNA.
HSSP; P01270; 1ZWB.
EMSEMDL; ENSWIGGO000059077; Mus musculus.
MGI; MGI:97799; Pth.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:00056179; F:hormone activity; IDA.
GO; GO:0006874; P:calcium ion homeostasis; TAS.
InterPro; IPR001415; Parathyrd.hrm.
InterPro; IPR001415; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; I.
PRAFF PTHR10541; Pthyrhorm_sub; I.
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PRAFF PTRSPO1822; PTH; 1.
  Length 115;
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   Lange C.A., Blumer K.J., Sather S.L., Johnson G.L., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
   Potential.
parathyroid hormone.
DA43FABBCB4E2FD9 CRC64;
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
   DB 2;
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  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
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  ch 46.3%; Score 75; DB 1 Similarity 58.1%; Pred. No. 0.33 18; Conservative 4; Mismatches
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   115 AA; 12825 MW;
   NUCLEOTIDE SEQUENCE OF 1-659.
TISSUE=Spleen;
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   NUCLEOTIDE SEQUENCE.
   Local Similarity
  SMART; SM00087;
   TISSUE=Thyroid
  32
   SEQUENCE
   Query Match
   Signal.
SIGNAL
   M3K1_MOUSE
  Best Loca
Matches
  RESULT 12
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ω

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GO; GO: 0030334; P:regulation of cell migration; IMP.

GO; GO: 000179; P:transforming growth factor beta receptor si. . .; IMP.

GO; GO: 0042060; P:wound healing; IMP.

R InterPro; IPR000731; Ser thr. pkinase.

BR InterPro; IPR003293; Ser thr. pkinase.

BR InterPro; IPR003903; UIM.

R InterPro; IPR003903; UIM.

BR InterPro; IPR001341; Znf SNIM.

BR InterPro; IPR001341; Znf SNIM.

BR InterPro; IPR001341; Znf SNIM.

BR Fam; PF00443; SNIM; 1.

BR Profons; PF00444; SNIM; 1.

BR Profons; PF00019; Prof. kinase; 1.

BR SNART; SM00120; S TKC; 1.

BR SNART; SM00184; RING; 1.

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BR PROSITE; PS0010; PROTEIN KINASE DOM; 1.

BR PROSITE; PS0010; PROTEIN KINASE DOM; 1.

BR PROSITE; PS0010; PROTEIN KINASE DOM; 1.

BR PROSITE; PS0010; PROTEIN KINASE ST; 1.
  autophosphorylation.

T-A: Loss of kinase activity and autophosphorylation. Fails to activate autophosphorylation. Fails to activate mAP2KI, MAP2KY, CHUK and IKBKB.
T-S: Loss of kinase activity and autophosphorylation.
T-S: Reduced kinase activity and autophosphorylation.
I-A: Loss of NF-kappa-B transcription factor activity and reduced ability to effect on AP-1 activity or activate MAP2KI, MAP2KY, NO effect on AP-1 activity or activate of F-A: Loss of AP-1 and NF-kappa-B transcription factor activity. Reduced ability to activate MAP2KI, CHUK and IKBKB.
M-A: Loss of AP-1 and NF-kappa-B transcription factor activity. Reduced ability to activate MAP2KI, MAP2KI, MAP2KI, CHUK and IKBKB.
M-A: Loss of AP-1 and NF-kappa-B transcription factor activity. Reduced ability to activate MAP2KI, MAP2KI, MAP2KI, CHUK and IKBKB.
M-A: Loss of AP-1 and NF-kappa-B transcription factor activity. Reduced ability to activate MAP2KI, MA
  activity and reduced ability to activate CHUK and IKBKR. No effect on NP. Kappa.B activity or activation of MAPZKI, MAPZK4, MAPZK7. Loss of binding to MAPZK4.
R-AR. Loss of AP-1 transcription factor activity, no effect on NP-Kappa-B
  T-AF Fails to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.
T->E: Loss of kinase activity and
  T->E: Loss of kinase activity and autophosphorylation.
T->S: Reduced kinase activity and
   Proton acceptor (By similarity).
ATP (By similarity).
Phosphothreonine.
Phosphothreonine.
   similarity)
   Protein kinase.
  RING-type.
ATP (By silpoly-Gly.
Pro-rich.
Pro-rich.
Poly-Ser.
  1393
   1403
   1489
361
487
1238
1238
149
291
426
1350
1350
1381
1381
  1381
  1381
  1393
  1393
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438
1230
25
25
74
417
1350
1253
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  1393
   1396
   1397
   1403
  1394
   1401
  Zinc-finger.
DOMAIN
   ZN_FING
ZN_FING
NP_BING
COMPBIAS
COMPBIAS
COMPBIAS
ACT
BINDING
MOD_RES
MOD_RES
MUTAGEN
  MUTAGEN
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                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
   EMBL; AF117340; AAD25049.1; -; mRNA.

EMBL; AB014614; BAA68978.1; -; mRNA.

EMBL; L13103; AAA97500.1; ALT INIT; mRNA.

EMBL; U23470; AAA95038.1; -; mRNA.

HSSP; Q16539; IKV1.

IIIAACI; P53349; ----

MGI; WG11346972; MGP3X1.

GO; GO:0001747; P:eye morphogenesis (sensu Mammalia); IMP.

GO; GO:0030838; P:positive regulation of actin filament polym. .; IMP.
  [6]
MUTION, INTERACTIONS WITH IKEKB AND MAP2K4, ENZYME REGULATION, AND MUTAGENESIS OF THR-1381; THR-1383; ISO-1384; PHE-1396; MET-1397; VAL-1401; LEU-1402; ARC-1403 AND GLY-1404.
Pubmed=14500727; DOI=10.1074/jbc.M304234200;
                MEDLINE=99455010; PubMed=10523642; Takamateu N., Suchioka K., Akechi M., Yamashita S., Takamateu N., Sugiyama K., Habi M., Nakabepu Y., Shiba T., Yamamoto K.-I.; Sugiyama K., Hibi M., Nakabepu Y., Shiba T., Yamamoto K.-I.; "JSAPI, a novel jun N-terminal protein kinase (JNK)-binding protein that functions as a scaffold factor in the JNK signaling pathway."; Mol. Cell. Biol. 19:7539-7548(1999).
  Johnson G.L., ^{\prime} A divergence in the MAP kinase regulatory network defined by MEK kinase and Raf.",
  [5]
ENZYME REGULATION, AND MUTAGENESIS OF THR-1381 AND THR-1393.
PubMed=9078<u>2</u>60;
  STRAIN=BALB/C; TISSUE=Brain;
MEDLINE=93227040; PubMed=8385802;
Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,
   Deak J.C., Templeton D.J.;
"Regulation of the activity of MEK kinase 1 (MEKK1) by
autophosphoxylation within the Kinase activation domain.";
Biochem. J. 322:185-192(1997).
  [4]
NUCLEOTIDE SEQUENCE OF 796-1493.
STRAIN=BALB/C; TISSUB=Heart;
Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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NUCLEOTIDE SEQUENCE OF 660-1493.
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Name=ETR3;
  Receptor.
SEQUENCE
  9
Receptor.
SEQUENCE
  Query Match
   RESULT 14

06T5K2 ORYSA

DG CFSK2, ORTSK2, ORT
  RESULT 15
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   R GO; GO: 0016620; C:membrane; IEA.

R GO; GO: 0016620; C:membrane; IEA.

R GO; GO: 0016524; F:ATP binding; IEA.

R GO; GO: 0016307; F:DNA binding; IEA.

R GO; GO: 0016301; F:kinase activity; IEA.

R GO; GO: 0001630; F:two-component response regulator activity; IEA.

R GO; GO: 0000155; F:two-component response regulator activity; IEA.

R GO; GO: 0000155; F:two-component seponse regulator activity; IEA.

R GO; GO: 0000155; F:two-component signal transduction system (p. . .; IEA.)

R GO; GO: 0000160; P:two-component signal transduction system (p. . .; IEA.)

R GO; GO: 0000160; P:two-component signal transduction system (p. . .; IEA.)

R GO; GO: 0000160; P:two-component signal transduction system (p. . .; IEA.)

R InterPro; IPR003648; ATPbind ATPase.

R InterPro; IPR003649; Response reg.

R Fam; PF01590; GAF; 1.

R Fam; PF01590; GAF; 1.

R Fam; PF01521; HisKA; I.

R PRODOM: PF0000032; Response reg; 1.

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10-FBB-2006 (TrEMBLrel. 29, Last annotation update)
10-FBB-2006 (Tracheophyta; Embryophyta; Embryophyta; Tracheophyta;
10-FBB-2006 (Tracheophyta; Liliopsida; Poales; Poaceae;
10-FBB-2006 (Tracheophyta; Liliopsida; Poales; Poaceae;
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GGGALGGSGA-> ALGGSG (in Ref. 2).
Wissing (in Ref. 2).
W -> W (in Ref. 2).
S -> C (in Ref. 2).
V -> A (in Ref. 2).
V -> L (in Ref. 3).
V -> L (in Ref. 3).
V -> L (in Ref. 3).
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  Score 73.5; DB 1; Length 1493;
Pred. No. 6.8;
4; Mismatches 10; Indels 19;
  Sasaki T., Margumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, clone:OJ1119 A01."; Submitted (AŪG-2001) to the EMBL/GenBank/DDBJ databases.
   CA65C9B7703C6BF9 CRC64;
   Sasaki T., Marsumoto T., Yamamoto K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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No. Government (1878).

No. Go
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7
  Gaps
  Gaps
   in rice during development, and in response to indole-3-acetic acid and silver ions.";
J. Exp. Bot. 55:547-556(2004).
EMBL; AY434735; AAR08915.1; -; mRNA.
  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
  <u>ب</u>
  3,
  PubMed=14754915; DOI=10.1093/jxb/erh055;
Yau C.P., Wang L., Yu M., Zee S.Y., Yip W.K.;
"Differential expression of three genes encoding an ethylene
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  836 AA; 92644 MW; 324D3E7F0B97A85A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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55.6%; Pred. No. 8.5;
tive 5; Mismatches
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Pred. No. 7.8;
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   6 GGGGGGGLNSMERV-EWLRKKLQDV 31
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55.6%;
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SMART; SM00388; Hi8KA; 1.
SMART; SM00448; REC; 1.
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QETSK2;
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Best Local Similarity
Matches 15; Conserv
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DT 01-ORT-2001 (TERMILE-E. 12, Last sequence update)
DT 01-ORT-2004 (TERMILE-E. 12, Last sequence update)
DT 01-ORT-2004 (TERMILE-E. 12, Last sequence update)
DT 01-ORT-2004 (TERMILE-E. 12, Last sequence update)
DE ENHylane receptor.like protein 2.
OFFAR astiva (Rice)
OFFAR astiva (Ric
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Search completed: November 21, 2005, 16:15:13 Job time : 148.5 secs

112 GGGGGGGLWSMDSIFRW--QKVSDL 136

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165, App 271, App 271, App 9, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

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Perfect score:

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OM protein

6

Scoring table:

Minimum DB & Maximum DB &

Database :

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APPLICAT: BIONebraska, Inc.
TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING
TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRICTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Merchant & Gould
STREET: 3100 Norwest Center, 90 S. 7th Street
CITY: Minneapolis
  Length 38;
US-09-536-785A-32
US-09-843-221A-165
US-09-643-221A-165
US-09-647-271
US-09-657-276-271
US-09-447-800-9
US-07-56-373-1
US-08-033-099-1
US-08-443-863-1
US-08-443-863-1
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US-08-447-651B-2
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Pred. No. 1.8e-05;
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07-DEC-1995
   APPLICALLA.

FILING DATE: 07-DEC-Lys-
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,530
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REGISTRATION NUMBER: 35,093
FERERENCE/DOCKET NUMBER: 8648.4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/156
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74.2%;
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STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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STATE: MA
COUNTRY: U.S.A.
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Best Local Similarity
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77.665 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-904-760B-1
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US-08-904-760B-14
US-08-904-760B-14
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
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   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
   Issued Patents AA:*
  seq length: 0
seq length: 200000000
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Match Length DB
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Score

Result

g ò

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   Gaps
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Sequence 37, Application US/08142551B
CENDEAL INSORMATION:
APPLICANT: S8146A; Harold E.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: Virginia
COUNTY: Alexandria
STATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Misk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Misk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION NUMBER: US 08/077,296
FILING DATE: 12-UN-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/869,219
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 12-UN-1993
FRIOR APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGRATING PATE:
DEFORMER OF SWEET OF GERALD F.
DEFORMER OF SWEET OF GERALD F.
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  Query Match 60.5%; Score 98; DB 1; Length 35; Best Local Similarity 71.0%; Pred. No. 2.8e-05; Matches 22; Conservative 2; Mismatches 7; Indels
   1 AVSEIGGGGGGGLNSMERVEWLRKKLODV 31
   NAME: Swiss, Gerald F.
REGISTRATION UNDRER: 30,113
REPERBUCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 844-7400
TELEPAX: (415) 844-7400
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acids
  % 308-142-551B-46

% Sequence 46, Application US/08142551B
% Settent No. 5814603
% GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
   NAME/KEY: Modified-site
| LOCATION: 35 | LOCATION: 36 | OTHER INFORMATION: from th; OTHER INFORMATION: from th; OTHER INFORMATION: residue, US-08-142-5518-37
  MOLECULE TYPE: protein
  unknown
  ropology:
  ò
  g
       °,
   ó
  NAME/KEY: Modified-site
LOCATION: 35
COTHER INFORMATION: /note= "Where "Xaa" is selected
COTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
COTHER INFORMATION: amide, or the sequence of amino acids comprising
COTHER INFORMATION: residues 35-84 of PTH."
   Gaps
       Gaps
   ;
0
       0
   RESULT 2
US-08-14-2-551B-34
US-08-142-551B-34
Sequence 34, Application US/08142551B
Patent No. 5814603
GENERAL INNORMATION:
APPLICANT: Oldenbrg, Kevin R.
APPLICANT: Oldenbrg, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
STREET: ADDRESSEE: Burne, Doane, Swecker & Mathis
STREET: Alexandria
CITY: Alexandria
STREET: Virginia
   Query Match 60.5%; Score 98; DB 1; Length 35; Best Local Similarity 71.0%; Pred. No. 2.8e-067; Indels Matches 22; Conservative 2; Mismatches 7; Indels
       7; Indels
  COUNTRY:

COUNTRY:
COUNTRY:
COUNTRY:
CONFUTER:
COMPUTER:
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
   1 SVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31
       1; Mismatches
  TYPE: amino acide TOPOLOGY: """."
  TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
       23; Conservative
   MOLECULE TYPE: protein
  Virginia
: US
   COUNTRY:
       Matches
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/note= "Where "Xaa" is selected
from the group consisting of Hol, Ho, a homoserine
amide, or the sequence of amino acids comprising
residues 35-84 of PTH."
   RESULT 6
US-08-142-551B-52

j Sequence 52, Application US/08142551B

j Sequence 100. 5814603

general INFORMATION:
   APPLICANT: Oldenburg, Kevin R.
   APPLICANT: Selick, Harold E.
   TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME NUMBER OF SEQUENCES: 132
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
   CITY: Alexandria
   STREET: Usignia
   COUNTRY: US
   Length 35;
  Indels
                                Ouery Match
59.3%; Score 96; DB 1; Le:
Best Local Similarity 71.0%; Pred. No. 4.9e-05;
Matches 22; Conservative 2; Mismatches 7;
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  1 SVSEIQLLGNLGKHLNSLERVEWLRKKLQDV 31
   NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REPREMENCE/DOCKET NUMBER: 000324-010
TELECHONE: (415) 854-7400
TELEPAN: (415) 854-7400
TELEPAN: (415) 854-7400
SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
  ZIE: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   NAME/KEY: Modified-site
  MOLECULE TYPE: protein
  ; LOCATION: 35
; OTHER INFORMATION: /
; OTHER INFORMATION: 6
; OTHER INFORMATION: a
; US-08-142-5518-40
   unknown
   TOPOLOGY: unbraced
Virginia
  Query Match
   ò
   엄
  ö
   /note= "Where "Xaa" is selected from the group consisting of Hol, Ho, a homoserine amide, or the sequence of amino acids comprising residues 35-84 of PTH."
  Gaps
  ;
0
   APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold B.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMPINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESSS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: Burns, Swecker & Mathis
STREET: 699 Prince Street
  COMPOUNDS WITH PTH ACTIVITY AND RECOMBINANT DNA VECTORS ENCODING SAME
   Query Match 60.5%; Score 98; DB 1; Length 35; Best Local Similarity 71.0%; Pred. No. 2.8e-05; Matches 22; Conservative 2; Mismatches 7; Indels
  COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 12-OCT-1993
PRIOR APPLICATION OPTA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/ACENT INFORMATION:
NAME: SW-180, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELEPHONE: (415) 854-8275
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LUNDED ARION ACENT SETION
TELEPOTH: 35 amino acids
   ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia COUNTRY: US
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   Sequence 40, Application US/08142551B Patent No. S814603 GENERAL INFORMATION:
   NAME/KEY: Modified-site
  TITLE OF INVENTION: COMPO
TITLE OF INVENTION: RECON
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
  MOLECULE TYPE: protein FEATURE:
  LOCATION: 35
OTHER INFORMATION: 0
OTHER INFORMATION: 0
OTHER INFORMATION: 0
   unknown
   TYPE: amino acid
TOPOLOGY: unknow
  CITY: Alexandria
   RESULT 5
US-08-142-551B-40
   US-08-142-551B-46
   ઠે
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Gaps

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1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  1 SVSEIQLLHNLGKGLNSLERVEWLRKKLQDV 31
  FILING DATE: 14-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/898,219

FILING DATE: 12-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/965,677

FILING DATE: 22-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: Swiss, Gerald F

REGISTRATION NUMBER: 30,113

REFERENCE/DOCKET NUMBER: 000324-010

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 854-8275

INFORMATION FOR SED ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGH: 35 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: unknown
  OTHER INFORMATION: Desamino Ala
US-09-447-800-6
  NAME/KEY: Modified-site
COATION: 35
COTHER INFORMATION: from th
COTHER INFORMATION: from th
COTHER INFORMATION: amide,
COTHER INFORMATION: residue,
US-08-142-5518-56
   Query Match
Best Local Similarity 71.04
Matches 22; Conservative
   MOLECULE TYPE: protein FEATURE:
   TYPE: PRT
ORGANISM: Homo sapiens
   NAME/KEY: MOD RES
   -09-447-800-6
  g
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   ö
  NAME/KEY: Modified-site

LOCATION: 35

OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: amide, or the sequence of amino acids comprising
US-08-142-551B-52
  Gaps
   .
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  US-08-142-551B-56
; Sequence 56, Application US/08142551B
; Sequence 56, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICAMT: Oldenburg, Kevin R.
; APPLICAMT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; STREET: 699 Prince Street
; STREET: 494 Prince Street
; CITY: Alexandria
; STATE: Usginia
  Query Match 59.3%; Score 96; DB 1; Length 35; Best Local Similarity 71.0%; Pred. No. 4.9e-09. Matches 22; Conservative 2; Mismatches 7; Indels Matches 22; Conservative 2; Mismatches 7; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,219
FILING DATE: 12-UN-1992
APPLICATION NUMBER: US 07/965,677
FILING DATE: 12-OCT-1992
ATTORNEY AGENT INFORMATION:
FILING DATE: 22-OCT-1992
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000124-010
TELEFOND NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000124-010
TELEFOND NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILLING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  1 SVSEIQLLHNLGGHLNSLERVEWLRKKLQDV 31
   ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  MOLECULE TYPE: protein FEATURE:
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   amino acid
  RESULT 7
US-08-142
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/note= "Where "Xaa" is selected from the group consisting of Hol, Ho, a homoserine amide, or the sequence of amino acids comprising residues 35-84 of PTH."
   Sequence 6, Application US/09447800
; Sequence 6, Application US/09447800
; Patent No. 6537965
; GRNRRAL INPORMATION:
APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: GARDELLA, THOWAS J.
; TITLE OF INVENTION: AMANOGE
; TITLE OF INVENTION: AMANOGE:
CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT PILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; RARLIER PILING DATE: 1999-11-25
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 6
; SEQ ID NO 6
; LENGTH: 33
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   Ouery March 58.6%; Score 95; DB 2; Length 33; Best Local Similarity 74.2%; Pred. No. 6.1e-05; Matches 23; Conservative 0; Mismatches 8; Indels
   59.3%; Score 96; DB 1; Length 35; 71.0%; Pred. No. 4.9e-05; tive 2; Mismatches 7; Indels
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INFORMATION FOR SEQ ID NO:
   US-09-843-221A-17
  LENGTH:
   g
   ò
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   ö
  GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISABI
APPLICANT: TAKASU, HISABI
APPLICANT: TAKASU, HISABI
APPLICANT: GRADELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMALOGS
FILE REFERENCE: 0609,4630001
CURRENT APPLICATION NUMBER: US/09/447,800
CURRENT PILING DATE: 1999-11-23
EARLIER PILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATECHIN Ver. 2.1
SEQ ID NO 5
LENGTH: 34
   0; Gaps
  APPLICANT: FUKUDA, Tsunchiko
APPLICANT: NAKAGAWA, Shizue
APPLICANT: HABASHITA, Junko
APPLICANT: TAKETOMI, Shigehisa
APPLICANT: TAKETOMI, Shigehisa
APPLICANT: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
  Query Match 58.6%; Score 95; DB 2; Length 34; Best Local Similarity 74.2%; Pred. No. 6.3e-05; Matches 23; Conservative 0; Mismatches 8; Indels
  COUNTRY.

ZIP: 02109

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DAY COMPATIBLE

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/044,536A
   DIKE, BRONSTEIN, ROBERTS & CUSHMAN
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  1 AVSEIQLMHNLGKHLNSMERVEWLRKKLODV 31
  Sequence 12, Application US/09044536A Patent No. 6025467 GENERAL INFORMATION:
  FILING DATE: 19-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/662,871
FILING DATE: 12-JUN-1996
ATTORNEY/AGENT INFORMATION:
   Sequence 5, Application US/09447800
Patent No. 6537965
  NAME: CONLIN, David G
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 465
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (617)523-3400
  NAME/KEY: MOD_RES
LOCATION: (1)
CTHER INFORMATION: Desamino Ala
US-09-447-800-5
   130 Water Street
   (617) 523-6440
  STREET: 130 Water Str
CITY: Boston
STATE: Massachusetts
   TYPE: PRT
ORGANISM: Homo sapiens
   ADDRESSEE:
  RESULT 10
US-09-044-536A-12
  US-09-447-800-5
   ઠે
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```

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US-09-843-221A-17

US-09-843-221A-17

US-09-843-221A-17

Sequence 17, Application US/09843221A

Patent No. 6756480

GENERAL INFORMATION:

APPLICANT: KOSTENUIK, PAUL

APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID #

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID #

FILE REFERENCE: A-665B

CURRENT APPLICATION NUMBER: G0/266, 673

PRIOR PELING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR PELING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PATENTING PATE: 1000-04-27

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 17
   GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHONN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID ITTLE OF INVENTION: RELATED PROTEIN
   ö
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   Gaps
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  ö
  Length 34;
  Ouery Match
58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels
  Length 34;
  LOCATION: 11
CTHER INFORMATION: /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12
   Query Match 58.0%; Score 94; DB 2; Le
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8;
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31
   1 SVSEIQLMHDXGKHLNSMERVEWLRKKLODV 31
  THER INFORMATION: modified human PTH
  US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Patent No. 6756480
   TYPE: PRT
ORGANISM: Artificial Sequence
   NAME/KEY: partial peptide LOCATION: 1..34
  NAME/KEY: Modified-site
                             TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
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```
GENERAL INFORMATION:
APPLICANT: KOSTENITA, PAUL
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIACEY, DAUL
APPLICANT: LIACEY, DAUL
APPLICANT: LIACEY, DAULATOR FOR RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC
TITLE OF INVENTION: RELATED PROTEIN
FILE REFREENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT APPLICATION NUMBER: 60/266,673
PRIOR APPLICATION NUMBER: 60/214,860
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PARENTIN VERSION 3.1
LENGTH: 34
   CTHER INFORMATION: Preferred embodiments - PTH
NAME/KEY: misc_feature
| NAME/KEY: misc_feature
| COCATION: (34)...(34)
| OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163
   ö
   RESULT 15
US-08-142-551B-43
Sequence 43, Application US/08142551B
Facent No. 5814603
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Oldenburg, Kevin R.
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
ADDRESSEE: Burns, Doane, Swecker & Mathis
  Query Match 58.0%; Score 94; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 8.3e-05; Matches 22; Conservative 1; Mismatches 8; Indels
  ADDRESSE: Burns, Dozone, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: Virginia
Z11: 2213
COMPUTER READABLE FORM:
MEDIUM TYPE: IDPDY disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: AND ADDRESSED ADDR
   1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
  TYPE: PRT
ORGANISM: Artificial Sequence
  ò
   d
  RESULT 13
US-09-643-221A-162
US-09-643-221A-162
Sequence 162, Application US/09643221A
Fatent No. 675640
Fatent No. 675640
Fatent No. 675640
FAPPLICANT: ROSTENUIK, PAUL
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE APPLICANT: ELACEY, DAVID LEE
TITLE OF INVENTION: MELATED PROTEIN
FILE REFERENCE: A-665B CO1-02-06
FURBRIT APPLICATION NUMBER: US/09/843,221A
CURRENT PILING DATE: 2001-04-26
FRIOR PELICATION NUMBER: 60/266,673
FRIOR PELICATION NUMBER: 60/206,673
FRIOR PELICATION NUMBER: 60/200,053
FRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VERIANCE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 162
LENGTH: 34
  NAWE/KEY: misc_feature; NGCATION: (34)...(34
   Gaps
  Gaps
   ö
  Query Match 58.0%; Score 94; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 8.3e-05; Matches 22; Conservative 1; Mismatches 8; Indels
   Query Match 58.0%; Score 94; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 8.3e-05; Matches 22; Conservative 1; Mismatches 8; Indels
  OTHER INFORMATION: Preferred embodiments - PTH
            FILE REFERENCE: A-665B
CURRENT APPLICATION WUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/214,860
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 18
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31
   ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18
   Sequence 163, Application US/09843221A Patent No. 6756480
  TYPE: PRT
ORGANISM: Artificial Sequence
  US-09-843-221A-163
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NAME: Swiss, Gerald F.

REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECHAUNICATION INCOMMATION:
TELEPHONE: (415) 854-7400
TELEPHONE: (415) 854-8275
INPORMATION FOR EXQ ID No: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 anino acids
TYBE: amino acids
TYBE: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEX: Modified-site
COATION: 35
OTHER INFORMATION: /note= "where "Xaa" is selected
OTHER INFORMATION: amide, or the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: residues 35-84 of PTH."
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   0; Gaps
   Query Match
Best Local Similarity 71.0%; Pred. No. 8.6e-05;
Matches 22; Conservative 2; Mismatches 7; Indels
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Search completed: November 21, 2005, 16:16:22 Job time : 34 secs

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18, Appl
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Appl
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Sequence 19, Appl
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-9161-928-6
US-10-892-025-20
US-09-843-221A-17
US-09-843-221A-162
US-09-843-221A-163
US-09-999-608-18
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US-10-899-608-163
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US-10-892-025-22
US-09-843-221A-27
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US-09-999-608-165
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Maximum Match 100%
Listing first 45 summaries
   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
   seq length: 0
seq length: 200000000
   US-09-475-158A-5
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Match Length
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Maximum DB
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   Database
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; Sequence 132, Application US/10997078
; Publication No. UG20050221444A1
; Sequence 132, Application No. UG20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Henguist, B.
; APPLICANT: Restoragen, Inc.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypept.)
; TITLE OF INVENTION: WHERE: 1627.010US1
; TITLE OF INVENTION NUMBER: US/10/997,078
; CURRENT APPLICATION NUMBER: US/10/997,078
; CURRENT APPLICATION NUMBER: US/10/997,078
; CURRENT APPLICATION NUMBER: US/10/997,078
; PRIOR FILING DATE: 2003-05-23
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
  ä
  OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.
                                 Sequence 271, App
Sequence 2, Appli
Sequence 20, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
   Sequence 6, Appli
Sequence 16, Appl
Sequence 161, App
  Gaps
Sequence
Sequence
Sequence
   Sequence
Sequence
  Sequence
  12;
  Length 89;
  Indels
  ---GGGLNSMERVEWLRKKLODV 31
  Sequence 19, Application US/10997762
; Sequence 19, Application US/2005027313A1
; GENERAL INFORMATION:
   APPLICANT: Seo, Jin Seog
   APPLICANT: Holmquist, Barton
   APPLICANT: Holmquist, Barton
   APPLICANT: Restoragen Inc.
   TITLE OF INFORTION: Polypeptide Cleavage Process
   FILE REFERENCE: 152.026US1
   CURRENT FILING DATE: 2004-11-24
  / Match 64.2%; Score 104; DB 5; I Local Similarity 59.0%; Pred. No. 6.7e-05; les 23; Conservative 1; Mismatches 3;
         ALIGNMENTS
   ORGANISM: Artificial Sequence
   5 IGGGGGG------
   JS-10-997-078-132
  US-10-997-078-132
  RESULT 2
US-10-997-762-19
  LENGTH: 89
  Query Match
   Best Loca
Matches
   ઠ
   g
```

Gaps

```
Sequence 6, Application US/10361928; Sequence 6, Application US/10361928; bublication No. US2003014420941; Sequence 6, Application No. US2003014420941; Sequence 6, Application No. US2003014420941; SAPERALLY INFORMATION:

APPLICANT: BRINGHURST, F. RICHARD; APPLICANT: GARDELLA, THOWAS J.

TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH); TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE; TITLE OF INVENTION: AMIAOGS; CURRENT APPLICATION NUMBER: US/10/361,928; CURRENT PILLING DATE: 2003-02-11; PRIOR APPLICATION NUMBER: 09/447,800; PRIOR PELLING DATE: 1999-11-25; NUMBER OF SEQ ID NOS: 10; SEQ ID NO 6; SEQ ID NO 6
  Length 141;
   / Match 58.6%; Score 95; DB 4; Length 33; Local Similarity 74.2%; Pred. No. 0.00031; les 23; Conservative 0; Mismatches 8; Indels
  Score 103; DB 5; Length 14
Pred. No. 0.00014;
1; Mismatches 3; Indels
   5 IGGGGGG------GGGLNSMERVEWLRKKLODV 31
   ; OTHER INFORMATION: A synthetic chimeric protein US-10-997-762-21
  1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE FREISEQ FOR Windows Version 4.0
SEQ ID NO 21
LENGTH: 141
  CTHER INFORMATION: Desamino Ala US-10-361-928-6
   TYPE: PRT
ORGANISM: Artificial Sequence
   Query Match 63.6%;
Best Local Similarity 56.1%;
Matches 23; Conservative
  TYPE: PRT
ORGANISM: Homo sapiens
  NAME/KEY: MOD_RES
LOCATION: (1)
  Query Match
  Matches
  Dp
   à
  ò
   ; OTHER INFORMATION: Amino acid sequence of a synthetic chimeric protein.
US-10-997-822-4
   Gaps
   14;
  14;
   Query Match 63.6%; Score 103; DB 5; Length 91; Best Local Similarity 56.1%; Pred. No. 9e-05; Matches 23; Conservative 1; Mismatches 3; Indels
  5; Length 91;
  3; Indels
  :|||||
48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLLQDV 88
   -----GGGLNSMERVEWLRKKLQDV 31
   48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88
   5 IGGGGGG------GGGLNSMERVEWLRKKLQDV 31
  US-10-997-822-4
; Sequence 4, Application US/10997822
; Publication No. US2005027314A1
; GENERAL INFORMATION:
; APPLICANT: Holmquist, B.
; APPLICANT: Strydom, D.
; APPLICANT: Gensalk, X.
APPLICANT: Gensalk, X.
APPLICANT: Gensalk, X.
; TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
; FILE REPERENCE: 1627.011013
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US/10/997,822
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US (0333,484
; PRIOR APPLICATION NUMBER: US (0333,484
; PRIOR APPLICATION NUMBER: US (0333,484
; PRIOR APPLICATION NUMBER: SON 50-5-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: RattSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 91
  Sequence 21, Application US/10997762
FUDILICALION NO. US20050227313A1
GENERAL INFORMATION:
APPLICANT: Sec. Jin Seog
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REPRENCE: 1627.026US1
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16468
   ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FATURE:
; PEATURE: INFORMATION: A synthetic chimeric protein
US-10-997-762-19
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Pred. No. 9e-05;
1; Mismatches
PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FABLESEQ for Windows Version 4.0
  TYPE: PRT
ORGANISM: Artificial Sequence
   Query Match
Best Local Similarity 56.1%;
Matches 23; Conservative
   RESULT 4
US-10-997-762-21
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Gaps

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셤
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   Sequence 20, Application US/10892025
Sequence 20, Application US/10892025
Publication No. US20050065071A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID
TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID
TITLE OF INVENTION: HORMONE FOR THE TREATMENT OF CONDITIONS CHARACTERIZED BY
TITLE OF INVENTION: HYPERPROLIFERATIVE SKIN CELLS
FILE REFERENCE: 3583.1000-001
CURRENT APPLICATION NUMBER: 2004-07-15
PRIOR APPLICATION NUMBER: 60/487,513
PRIOR FILING DATE: 2003-07-15
  ö
  ö
  Gaps
   NHR; wherein R is hydrogen or a linear or branched chain alkyl, acyl or aryl group
   0; Gaps
   Y; where Y is X, His-X, His-Asn-X, or
His-Asn-Phe-X; where X is OR or NHR; and R is
hydrogen or a linear or branched chain alkyl, acyl
or aryl group
  is selected from the group consisting of Met, norisoleucine, and a hydrophobic amino acid
  ;
   Query Match 58.6%; Score 95; DB 4; Length 34; Best Local Similarity 74.2%; Pred. No. 0.00032; Matches 23; Conservative 0; Mismatches 8; Indels
   Query Match 58.0%; Score 94; DB 5; Length 31; Best Local Similarity 71.0%; Pred. No. 0.00039; Matches 22; Conservative 1; Mismatches 8; Indels
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  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  1 SVSEIQLXHNLGKHLNSMERVEWLRKKLQDV 31
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  NUMBER OF SEQ ID NOS: 42
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                   PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 1998-11-25
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SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 5
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ORGANISM: Homo sapiens
   TYPE: PRT
ORGANISM: Homo sapien
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CTHER INFORMATION: US-10-892-025-20
   LOCATION: 8
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OTHER INFORMATION:
  OTHER INFORMATION: OTHER INFORMATION:
  FEATURE:
NAME/KEY: MOD_RES
   NAME/KEY: VARIANT
  FEATURE:
NAME/KEY: SITE
  NAME/KEY: SITE
   US-10-892-025-20
  LOCATION:
   ઠે
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   В
```

```
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LAGEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
TITLE OF INVENTION: WISHATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: 08/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR PILING DATE: 2000-06-66,673
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-37
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 17
  Sequence 18, Application US/09843221A
Publication No. US20030039654A1
Publication No. US20030039654A1
APPLICANT: NOSTENDIK, PAUL
APPLICANT: LIU, CHUAN FA
APPLICANT: LIU, CHUAN FA
TITLE OF INVENTION: RELATED PROTEIN
   ö
   ö
  Gaps
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   ;
   ;
  Length 34;
  Length 34;
   Query Match
58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels
   Indels
   Query Match
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8;
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
  1 SVSEIQLMHNRGKHLNSMERVEWLRKKLODV 31
  TILIB REPERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR PELING DATE: 2001-02-06
PRIOR PILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 18
  1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
  ) OTHER INFORMATION: modified human PTH US-09-843-221A-18
   ; OTHER INFORMATION: modified human PTH
US-09-843-221A-17
Sequence 17, Application US/09843221A Publication No. US20030039654A1 GENERAL INFORMATION:
   ORGANISM: Artificial Sequence
  ORGANISM: Artificial Sequence
   APPLICANT: KOSTENUIK, PAUL
  US-09-843-221A-18
   FEATURE:
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US-00-999-608-17

US-00-999-608-17

US-00-999-608-17

US-00-999-608

Publication No. US20050124537A1

GEGRACHIT NORMARIAN

APPLICANT: GEGG, COLIN V

APPLICANT: GEGG, COLIN V

APPLICANT: GEGG, COLIN V

APPLICANT: MINSTLER, OLAF BORIS

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID

TITLE OF INVENTION: MODULATORS OF RECEPTORS

FILE REFERENCE: A-665C

TITLE OF INVENTION: MODULATORS OF RECEPTORS

FILE REPERENCE: A-665C

CURRENT FILING DATE: 2002-03-11

FRIOR PLILING DATE: 2001-04-26

FRIOR APPLICATION NUMBER: US 60/266,673

FRIOR PLING DATE: 2001-02-06

FRIOR PLING DATE: 2001-02-06

FRIOR PLING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 193

SEQ ID NOS: 193

SEQ ID NO 17

LINGUIL SAFERMENT PLING DATE: PARENTHYROID HORMONE AND PARATHYROID

LINGUIL SAFERMENT PLING DATE: 2001-04-26

FRIOR FILING DATE: 2001-04-26

FRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 193

SEQ ID NO 17

LINGUIL SAFERMENT PLINGUIL VERSION 3.2
   US-09-999-608-18

Sequence 18, Application US/0999608

Publication No. US20050124537A1

GENERAL INFORMATION:
APPLICANT: KOSTERUIK. PAUL
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: HINTLE OF INVENTION: HORMONE AND PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: MODULATORS OF RECEPTORS
CURRENT APPLICATION NUMBER: US/09/999, 608
CURRENT FILING DATE: 2001-03-11
PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06
; LOCATION: (34)...(34)
; OTHER INFORMATION: Optional linker and Pc domain attached at the C-terminus
US-09-843-221A-163
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  ö
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ORGANISM: Artificial Sequence
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US-09-843-21A-162

US-09-843-21A-162

Sequence 162, Application US/09843221A

Publication No. US20030039654A1

Sequence 162, Application US/09843221A

Publication No. US20030039654A1

APPLICANT: ILU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

CURRENT APPLICATION NUMBER: US/09/843,221A

CURRENT FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARK: PatentIn Version 3.1

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US-09-643-221A-163

Sequence 163, Application US/09843221A

Publication No. US20030039654A1

SEGNERAL INFORMATION:

APPLICANT: LACEY, DAVID LEE

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HILL OF INVENTION RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION WUMBER: US/09/843,221A

CURRENT FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-38

PRIOR FILING DATE: 3000-06-38

PRIOR FILING DATE: 3000-06-38

PRIOR FILING DATE: 2000-06-38

PRIOR FILING DATE: 3000-06-38

   OTHER INFORMATION: Preferred embodiments - PTH
NAME/KEY: misc_feature
LOCATION: (34)~.(34)
OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162
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OTHER INFORMATION: Preferred embodiments - PTH
NAME/KEY: misc_feature
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ORGANISM: Artificial Sequence
   ORGANISM: Artificial Sequence
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COLIN V.
   US-09-999-608-163
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   g
  ð
   APPLICANT: GEGG, COLIN V.
APPLICANT: JAROSINSKI, MARK ANTHONY
APPLICANT: JAROSINSKI, MARK ANTHONY
APPLICANT: TINSTLER, OLDER BORIS
TITLE OF INVENTION: MODULATIONS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
   NAME/KEY: misc_feature

| LOCATION: 34)...(34)

| OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

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  Query Match 58.0%; Score 94; DB 3; Length 34; Best Local Similarity 71.0%; Pred. No. 0.00042; Matches 22; Conservative 1; Mismatches 8; Indels
   OTHER INFORMATION: Preferred embodiments - PTH
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CURRENT APPLICATION NUMBER: US/09/999,608
CURRENT FILING DATE: 2002-03-11
PRIOR PRILING DATE: 2001-04-26
PRIOR PRILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-06-673
PRIOR FILING DATE: 2001-06-68
PRIOR FILING DATE: 2000-06-28
SOFTWARE: PARCHING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 193
SOFTWARE: PARCHIN VERSION 3.2
SOFTWARE: PARCHIN VERSION 3.2
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: US 60/200,053
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 34
  ; OTHER INFORMATION: modified human PTH
US-09-999-608-18
  Sequence 163, Application US/0999608
Publication No. US20050124537A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
  Sequence 162, Application US/0999608
Publication No. US20050124537A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
  TYPE: PRT
ORGANISM: Artificial Sequence
   ORGANISM: Artificial Sequence
   US-09-999-608-163
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  FEATURE:
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APPLICANT: JOSOSINST, WARK ANTHONY
APPLICANT: JOSOSINST, WARK ANTHONY
APPLICANT: JOSOSINST, WARK ANTHONY
APPLICANT: JOSOSINST, WARK ANTHONY
APPLICANT: KINSTER, OLDA FORE
TITLE OF TRYBETION: HORMONE-RELATED PROTEIN
FILE OF TRYBETION: HORMONE-RELATED PROTEIN
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FRICK APPLICATION NUMBER: US 09/843,221
FRIOR PILING DATE: 2002-03-11
FRIOR PILING DATE: 2002-06-26
FRIOR PILING DATE: 2000-06-26
FRIOR PILING DATE: 2000-06-28
FRIOR PILING DATE: 2000-04-27
FRIOR FILING DATE: 2000-04
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Sequence 3, Appli
Sequence 21, Appli
Sequence 21, Appl
Sequence 64, Appli
Sequence 7, Appli
Sequence 32, Appli
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  Sequence
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-105-943-20
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US-11-077-550-50
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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26 48 29.6 10 1 US-10-512-184-44 Sequence 44, Appl 27 48 29.6 15 1 US-10-495-664-1 Sequence 1, Appli 29 48 29.6 15 1 US-10-97-9-111 Sequence 1, Appli 30 48 29.6 15 1 US-10-97-9-111 Sequence 11, Appli 30 48 29.6 15 7 US-11-144-248-60 Sequence 60, Appl 31 48 29.6 20 7 US-11-165-943-48 Sequence 32, Appl 33 48 29.6 251 1 US-10-512-184-31 Sequence 31, Appl 36 48 29.6 259 1 US-10-512-184-31 Sequence 31, Appl 36 48 29.6 259 1 US-10-912-184-31 Sequence 31, Appl 37 48 29.6 313 1 US-10-512-184-69 Sequence 72, Appl 39 48 29.6 313 1 US-10-512-184-69 Sequence 67, Appl 48 29.6 320 1 US-10-512-184-69 Sequence 67, Appl 48 29.6 320 1 US-10-512-184-69 Sequence 67, Appl 48 29.6 320 1 US-10-512-184-69 Sequence 67, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 67, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 67, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-70 Sequence 67, Appl 48 29.6 329 1 US-10-512-184-70 Sequence 67, Appl 48 29.6 329 1 US-10-512-184-70 Sequence 67, Appl 48 29.6 329 1 US-10-512-184-69 Sequence 70, Appl 48 29.6 329 1 US-10-512-184-70 Sequence 67, Appl 49 29.6 329 1 US-10-512-184-70 Sequence 70, Appl 49 29.6 329 1 US-10-512-184-70 Sequence 67, Appl 40 29.6 329 1 US-10-512-184-70 Sequence 67, Appl 40 29.6 329 1 US-10-512-184-90 Sequence 67, Appl 40 29.6 329 1 US-10-512-184-90 Sequence 67, Appl 40 29.6 329 1
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## ALIGNMENTS

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  Sequence 3, Application US/10975798
| Sequence 3, Application Wo. US20050250090A1
| GENERAL INFORMATION:
| APPLICANT: Eddy Chaplan
| APPLICANT: Adriene Dubin
| APPLICANT: Saidy Chaplan
| APPLICANT: Saidy Chaplan
| APPLICANT: Saidy Chaplan
| TITLE OF INVENTION: WITH SK2 CHANNELS
| TITLE OF INVENTION: WITH SK2 CHANNELS
| TITLE OF INVENTION WIMBER: US/10/975,798
| CURRENT APPLICATION WUMBER: US/10/975,798
| CURRENT APPLICATION WUMBER: US/10/975,798
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(Sequence 21, Application US/11004057)

(Sequence 21, Application US/11004057)

(Sequence 21, Application No. US2005024846A1)

(Sequence 10, Application No. US2005024846A1)

(SEDEREL INFORMATION)

(SEDEREL INFORMATION)

(SETULE OF INVENTION)

(SETULE OF INVENTION)

(CURRENT APPLICATION NUMBER: US/11/004,057)

(CURRENT PILING DATE: 2004-12-02)

(CURRENT FILING DATE: 2000-05-10)

(SEQ ID NOS: 21)

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  Gaps
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34.9%; Score 56.5; DB 7; Length 1493;
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US-11-004-057-21
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US-10-975-798-3
; ORGANISM: Homo sapiens
US-10-975-798-4
   580
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US-10-975-798-3
   ò
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  à
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RESULT 5

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8
   셤
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  ö
   APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1G128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
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OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
US-11-060-659-32
   OTHER INFORMATION: Description of Artificial Sequence:synthetic poly OTHER INFORMATION: Gly flexible linker
   APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Holland, Sacha J.
APPLICANT: Holland, Sacha J.
APPLICANT: Au, Weiduan
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
FILE REFERENCE: 021044-008310US
CURRENT APPLICATION NUMBER: US/11/060,659
CURRENT FILING DATE: 2005-02-16
PRIOR FILING DATE: 2004-02-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2. 1
TITLE OF INVENTION: (KIAA0660) cDNA
SEQ ID NO 32
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  CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
; Sequence 32, Application US/11060659; Publication No. US20050250163A1; GENERAL INFORMATION:
  ORGANISM: Artificial Sequence
  Desnoyers, Luc
Filvacoff, Ellen
Gao, Wei-Diang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
  Stewart, Timothy A.
   APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
   Watanabe, Colin K
   Sherwood, Steven
   Query Match 33.3
Best Local Similarity 100.
Matches 9; Conservative
   Smith, Victoria
   Tumas, Daniel
  6 GGGGGGGG 14
   NAME/KEY: MOD_RES
  US-10-131-826A-532
   APPLICANT:
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   ò
  유
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US-11-065-943-20

Sequence 20, Application US/11065943

Sequence 20, Application US/11065943

Publication No. US20050250131A1

GENERAL INFORMATION:

APPLICANT: USETIN, JEAN-LUC

APPLICANT: VICHER-GUERE, SOPHIE

APPLICANT: VICHER-GUERE, SOPHIE

APPLICANT: VICHER-GUERE, SOPHIE

APPLICANT: WITHON: WATHONS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

ITILE OF INVENTION: WATHONS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

TITLE OF INVENTION: WATHONS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

TITLE OF INVENTION: WINDER: US/11/065,943

CURRENT FILING DATE: 2004-02-25

PRIOR APPLICATION NUMBER: US 10/787,219

PRIOR PILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

LEMACHAL: CALLED AND ALTER AND ALTER AND APPLICATIONS OF THE SAME

SEQ ID NO 20

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SEQ ID NO 20

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SEQ ID NO 20

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PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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PRIOR PLIOR APPLICATION NUMBER: 60/059588
PRIOR PLING DATE: 1997-09-19
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   US-11-065-943-22
; Sequence 22, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
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50.0%;
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  ĠĠĠĠĠĠĠSPĸAĽĖEAPW
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 100:
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   US-10-131-826A-532
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US-11-065-943-30

US-11-065-943-30

Sequence 30, Application US/11065943

Publication No US20050250131A1

GENERAL INFORMATION:

APPLICANT: USCHIRE-GUEERE, SOPHIE

APPLICANT: VICHIRE-GUEERE, SOPHIE

APPLICANT: PERRIS, STEPHANE

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

FILE REPERENCE: 564246020XCIP

TITLE OF INVENTION: UNMER: US/11/065,943

CURRENT FILING DATE: 2005-02-25

FROM FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 30

SEQ ID NO 30
   US-11-US-2943-Z8

Sequence 28, Application US/11065943

Publication No. US20050250131A1

Sequence 28, Application US/11065943

Publication No. US20050250131A1

SEQUENCE INFORMATION:

APPLICANT: UICHIR-GUEREE, SOPHIE

APPLICANT: VICHIR-GUEREE, STEPHANE

TITLE OF INVENTION: WAETHOUS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: WAETHOUS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

TITLE OF INVENTION WHERE: US/11/065,943

CURRENT FILING DATE: 2005-02-25

PRIOR FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PATENTIN VERBION 3:3

SEQ ID NO 28

TABRITHS 562

TABRITHS SECOND NOS: 106

SOFTWARE: PATENTIN VERBION 3:3

SEQ ID NO 28

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CURRENT FILING DATE: 2005-02-25
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PRIOR FILING DATE: 2004-02-27
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US-11-065-943-24

i Sequence 24, Application US/11065943

i Publication No. US20050250131A1

i GENERAL INFORMATION:

i APPLICANT: USTIN, USAN-LUC

i APPLICANT: PERRIS, STEPHANE

i TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

i TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: UNMERR: US/11/065,943

CURRENT APPLICATION NUMBER: US/11/065,943

FRICR REPERING DATE: 2004-02-25

PRICR PLING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE PATENTIN VERSION 3.3

TANGEN OF 24

TANGEN OF 24
APPLICANT: JESTIN, JEAN-LUC
APPLICANT: VICHIERE-GUERERE, SOPHIE
APPLICANT: FERRIS, STEPHANE
TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: VARANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTICS ACTIVITIES,
TITLE OF INVENTION: WETHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
FILE REFERENCE: 266426USOXCIP
CURRENT PEPPLICATION NUMBER: US, 11/065, 943
CURRENT FILING DATE: 2006-02-25
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin version 3.3
EEQ ID NO 22
  Sequence 26, Application US/11065943
| Publication Wo. US20050250131A1
| GENERAL INFORMATION:
| APPLICANT: JESTIN, JEAN-LUC
| APPLICANT: DESTIN, JEAN-LUC
| APPLICANT: FERRIS, SCPHIE
| APPLICANT: FERRIS, STEPHANE
| TITLE OF INVENTION: WETHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
| TITLE OF INVENTION: WALRAYS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
| TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
| FILE REFERENCE: 266426USOXCIP
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33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels
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Best Local Similarity 50.0%; Pred. No. 1.4;
Matchea 9; Conservative 2; Mismatchea 7; Indels
Matchea 9; Conservative 2; Mismatchea 7; Indels
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; ORGANISM: Thermus aquaticus
US-11-065-943-22
   TYPE: PRT

ORGANISM: Thermus aquaticus
US-11-065-943-24
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Sequence 32, Application US/11065943

Fublication No. US20050250131A1

GENERAL INFORMATION

APPLICANT: JESTIN, JEAN-LUC

APPLICANT: VICHIER-GUERE, SOPHIE

APPLICANT: VICHIER-GUERE, SOPHIE

APPLICANT: VICHIER-GUERE, SOPHIE

APPLICANT: VICHIER-GUERE, STEPHANE

ITILE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

TITLE OF INVENTION: WETHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

CURRENT APPLICATION NUMBER: US/11/065,943

CURRENT FILING DATE: 2005-02-25

PRIOR PPLICATION NUMBER: US 10/787,219

PRIOR PPLING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SSOFTWARE: PALENTIN VERSION 3.3

SEQ ID NO 32

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; ORGANISM: Thermus aquaticus
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November 23, 2005, 22:00:32 ; Search time 242.667 Seconds (without alignments) 2554.189 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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   geneseqn2005s:*
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Maximum Match 100%
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Maximum DB seq length: 200000000
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93
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Perfect score:
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  Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description              |          | _        | Aaa51731 PTH funct | Aat73910 Synthetic | Adg93179 Novel exp | Adj65857 PTH pepti | Adw14377 Human par |          | Adj65858 PTH pepti | Adw14375 Human par | Adg93260 Novel exp | Aat34865 Plasmid p | Adg93181 Novel exp | Adj65859 PTH prote | Adj65913 Tandem po | Adf90345 Chimeric |          | Adj87051 Nucleotid | Adg93252 Novel exp |
|-----------|--------------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|----------|--------------------|--------------------|
| SUMMARIES | ΩI                       | AAA51729 | AAA51730 | AAA51731           | AAT73910           | ADG93179           | ADJ65857           | ADW14377           | ADG93180 | ADJ65858           | ADW14375           | ADG93260           | AAT34865           | ADG93181           | ADJ65859           | ADJ65913           | ADF90345          | ADJ65899 | ADJ87051           | ADG93252           |
|           | рв                       | Э        | ٣        | m                  | 7                  | 12                 | 12                 | 13                 | 12       | 12                 | 13                 | 12                 | 7                  | 12                 | 12                 | 12                 | 12                | 12       | 12                 | 12                 |
|           | Query<br>Match Length DB | 93       | 93       | 93                 | 152                | 102                | 102                | 102                | 111      | 111                | 111                | 117                | 168                | 252                | 252                | 264                | 276               | 276      | 276                | 282                |
| de        | Query                    | 100.0    | 89.7     | 79.4               | 76.6               | 74.8               | 74.8               | 74.8               | 74.8     | 74.8               |                    | •                  | 74.8               | 74.8               | 74.8               | 74.8               | 74.8              | 74.8     | 74.8               | 74.8               |
|           | Score                    | 93       | 83.4     | 73.8               | 71.2               | 9.69               | 9.69               | 9.69               | 9.69     | 9.69               | 9.69               | 9.69               | 69.6               | 69.6               | 69.6               | 69.6               | 69.6              | 9.69     | 69.6               | 9.69               |
|           | Result<br>No.            |          | 7        | 9                  | 4                  | ហ                  | 9                  | 7                  | 80       | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                | 17       | 18                 | 19                 |

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

| PTH      | Adj65900 PTH DNA 8 |          | Adj65915 Tandem po | Adj65917 Tandem po | ^        | Aas19702 DNA encod | Adv69494 Human par | Adv69502 Human par | Adg48030 Human PTH | Adg48059 Human PTH | Adg68786 Human mut | Aag89920 Recombina | Aat80383 rPTH codi | Aaq89923 Expressio | Adw80822 DNA encod |          | AaaS1455 PCpB-LVPR | Aaa51454 PCpB-IEGR | m        | m        | Aaa51456 PCpB-VIPR | AaaS14S7 PCpB-DQVD | ~        | Aaq55301 Truncated | Aaq55302 gp55-Asn- |
|----------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|
| ADJ65901 | ADJ65900           | AAT34866 | ADJ65915           | ADJ65917           | ADF90347 | AAS19702           | ADV69494           | ADV69502           | ADG48030           | ADG48059           | ADG68786           | AAQ89920           | AAT80383           | AAQ89923           | ADW80822           | AAA51452 | AAA51455           | AAA51454           | AAA51453 | AAA51459 | AAA51456           | AAA51457           | AAA51458 | AAQ55301           | AAQ55302           |
| 12       | 12                 | 7        | 12                 | 12                 | 12       | 9                  | 13                 | 13                 | 12                 | 12                 | 12                 | ~                  | ~                  | 7                  | 13                 | ٣        | m                  | m                  | ო        | ო        | m                  | m                  | m        | ~                  | 7                  |
| 291      | 291                | 294      | 321                | 420                | 426      | 528                | 108                | 114                | 489                | 489                | 489                | 141                | 141                | 207                | 145                | 405      | 408                | 408                | 411      | 414      | 417                | 423                | 435      | 728                | 945                |
| 74.8     | 74.8               | 74.8     | 74.8               | 74.8               | 74.8     | 74.8               | 73.1               | 73.1               | 73.1               | 73.1               | 73.1               | 68.6               | 9.89               | 9.89               | 6.99               | 64.5     | 64.5               | 64.5               | 64.5     | 64.5     | 64.5               | 64.5               | 64.5     | 61.7               | 61.7               |
| 9.69     | 9.69               | 9.69     | 9.69               | 9.69               | 9.69     | 9.69               | 68                 | 68                 | 68                 | 68                 | 68                 | 63.8               | 63.8               | 63.8               | 62.2               | 09       | 09                 | 9                  | 09       | 9        | 09                 | 9                  | 09       | 57.4               | 57.4               |
| 20       | 21                 | 22       | 23                 | 24                 | 25       | 56                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36       | 37                 | 38                 | 39       | 40       | 41                 | 42                 | 43       | 44                 | 45                 |
|          |                    |          |                    |                    |          |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |          |                    |                    |          |          |                    |                    |          |                    |                    |

## ALIGNMENTS

RESULT 1 AAA51729

PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss. PTH functional domain conjugate peptide PG5 coding sequence. Gardella TJ, Kronenberg HM, Potts JT, Jueppner H; Location/Qualifiers
1. .93
/\*tag= a
/product= "PG5" AAA51729 standard; RNA; 93 BP. 99WO-US031108. 98US-0114577P. 31-OCT-2000 (first entry) (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M. (POTT/) POTTS J T. (JUEP/) JUEPPNER H. WPI; 2000-452384/39. P-PSDB; AAY96973. WO200039278-A2 31-DEC-1998; Homo sapiens. Synthetic. 30-DEC-1999; 06-JUL-2000. AAA51729; Key 

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Synthetic.
  61
   AAA51731;
  (JUEP/)
   RESULT 3
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   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an anino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHRP which avoids the need for regular injections to treat osteoporosis
   9
   9
  1 GCUGUUUCCGAAAUCCAGCUGAUGCACGUGGUGGUGGUGGUCUGAACUCCAUGAACGU
   1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGU
   New compound comprising an amino terminal signaling functional domain
  PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss.
  PTH functional domain conjugate peptide PG7 coding sequence.
   Score 93; DB 3; Length 93;
Pred. No. 1e-22;
   0; Indels
  Sequence 93 BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;
   Potts JT, Jueppner H;
   GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  guugaaugecueceuaaaaacuecaedaceuu 93
  0; Mismatches
   Location/Qualifiers
   1. .93
/*tag= a
/product= "PG7"
                       Claim 14; Fig 1; 119pp; English
   Query Match
Best Local Similarity 100.0%;
Matches 93; Conservative 0;
  AAA51730 standard; RNA; 93 BP.
   Gardella TJ, Kronenberg HM,
   99WO-US031108.
  98US-0114577P
  31-OCT-2000 (first entry)
  (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M.
  WPI; 2000-452384/39.
P-PSDB; AAY96975.
  POTTS J T.
JUEPPNER H.
  WO200039278-A2.
   31-DEC-1998;
   30-DEC-1999;
   Homo sapiens
Synthetic.
   06-JUL-2000
  AAA51730;
  (KRON/) H
(POTT/) E
(JUEP/)
   RESULT 2
AAAS 1730
LD AAAS 1730
XX AAAS 231-C
XX XX PTH, WW PT
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   ò
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (FTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the FTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH PT Which avoids the need for regular injections to treat osteoporosis
  9
linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   1 ecueuuucceaaauccagcugaugcacegugguggugguggucugaacuccauggaaceu
   0; Gaps
   PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss.
  PTH functional domain conjugate peptide PG9 coding sequence.
  Score 83.4; DB 3; Length 93;
Pred. No. 2.5e-19;
0; Mismatches 6; Indels
  Sequence 93 BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;
  Jueppner H;
   93
  61 GUUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  Potts JT,
  Location/Qualifiers
   Claim 14; Fig 1; 119pp; English.
   1. .93
/*tag= a
/product= "PG9"
   89.7%;
  AAAS1731 standard; RNA; 93 BP
  Gardella TJ, Kronenberg HM,
   99WO-US031108.
  98US-0114577P.
   31-OCT-2000 (first entry)
   Query Match
Best Local Similarity 93.5;
Matches 87; Conservative
  (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
  WPI; 2000-452384/39.
P-PSDB; AAY96974.
   JUEPPNER H.
  WO200039278-A2
  Homo sapiens.
   30-DEC-1999;
  31-DEC-1998;
  06-JUL-2000.
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Compounds of the structure or formula S-(1), n-B, R 1-S-(1), n-R or S-(1), n-R or S-(1
   Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; endoproteinase LysC; ds.
  9
   ccueutucceaaauceueeueeueeueeueeueeueeuceueeucueaacuccaueeaaceu 60
   /label= sticky_end
/note= "5' end of complementary strand overhangs 3' end
of present strand by sequence 5'-TCGA-3'"
6. .152
                New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGU
  Gaps
  .
0
  Score 73.8; DB 3; Length 93;
Pred. No. 6e-16;
0; Mismatches 12; Indels
  Synthetic oligonucleotide encoding linker and PTH 1-37.
   Sequence 93 BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;
  61 GUUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   cocation/Qualifiers
   (BOEF ) BOEHRINGER MANNHEIM GMBH.
   Claim 14; Fig 1; 119pp; English.
  AAT73910 standard; DNA; 152 BP
  96WO-EP004850.
  95DE-01042702.
  79.48;
  Local Similarity 87.1%;
les 81; Conservative
   (first entry)
   Ω
  ...4
*tag=
  /*tag=
  (revised)
  Homo sapiens
  misc_feature
  WO9718314-A1
  06-NOV-1996;
   25-MAR-2003
30-JAN-1998
  22-MAY-1997
  Synthetic
  AAT73910;
  Query Match
  RESULT 4
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The present sequence, which encodes a linker and the parathyroid hormone cc 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains the Missing kinaparidin [SA) sequence, to give pSA-EK-PTH. pSA-EK-PTH and the Lacig repressor plasmid pUBS500 were used to transform E. C PTH and the Lacig repressor plasmid pUBS500 were used to transform E. C coli K12 RM82. The transformants were grown, with IPTG induction, in C medium containing kanamycin and amplicilin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidian hydrochloride, and creatured by dilution in pH 7 phosphate buffer. The solution was clamm of immobilised iminobiotin. The purified and purified on a column of immobilised iminobiotin column followed by chromatography on a fragment removal on an iminobiotin column followed by chromatography on a fractogel and reversee phase PHPC. The endoproteinase Lysc cleaves the fractogel and reversee phase PHPC. The endoproteinase Lysc cleaves the fractogel and reversee phase PHPC. The endoproteinase Lysc cleaves the the linker, i.e. not at Lys residues in SA. (Updated on 25-MAR-2003 to correct PR field.)
   2 cuguruccgaaauccagcugaugcacguggugguggugguggucgugaacuccauggaacgug 61
  Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and parathyroid hormone production.
   Gaps
   Novel expression cassette-related polypeptide-encoding DNA SeqID60.
  .;
0
   Score 71.2; DB 2; Length 152;
Pred. No. 5.7e-15;
   Indels
  expression cassette, high yield polypeptide production;
tandem polypeptide; inclusion body; gene; ds.
  Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;
   ::|||:|||:|||:|||:|||||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  19; Mismatches
   Luan P,
   Bb.
   Example 2; Fig 2; 37pp; German.
   23-MAY-2003; 2003WO-US016643.
   24-MAY-2002; 2002US-0383370P.
   Match 76.6%;
Local Similarity 65.2%;
les 60; Conservative 1
   ADG93179 standard; DNA; 102
  11-MAR-2004 (first entry)
   Harley S, Williams JA,
  RESTORAGEN INC
HARLEY S.
   WPI; 2004-035128/03
   WPI; 1997-289290/26.
P-PSDB; AAW21946.
   WO2003100021-A2.
  Unidentified
   04-DEC-2003.
Kopetzki E;
  ADG93179;
  Query Match
   (REST-)
   (HARL/)
   Matches
  RESULT 5
   ADG93175
  DX LI X B X 
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The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADWI4376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADWI4378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the PTH 1-34 apptide.
   2 CUGUIUCCGAAAUCCAGCUGAUGCACGUGGUGGUGGUGGUGGUCCGAACUCCAUGGAACGUG 61
  inclusion body when expressed in a cell. The present DNA sequence encod a peptide which may be used in the construction of a tandem polypeptide of the invention.
  2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   2 cuguuccgaaauccagcugaugcacgguggugguggugguggugguggaacuccauggaacgug
   0; Gaps
   Production of reorganized human parathyroid hormone 1-34 peptide
   ö
   74.8%; Score 69.6; DB 13; Length 102; 63.0%; Pred. No. 1.9e-14; tive 20; Mismatches 14; Indels 0;
   Query Match
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0.
   Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.
   ds; parathyroxin; recombinant protein; protein engineering.
  Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;
  Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;
   ŝ
   (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD
   ::|||:|||:|||:|||
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   TIGAATGGCTGCGTAAAAACTGCAGGACGTT 93
  UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  Disclosure; SEQ ID NO 3; 25pp; Chinese.
  BP.
   12-DEC-2001; 2001CN-00142627.
  12-DEC-2001; 2001CN-00142627
  ADW14377 standard; DNA; 102
  Local Similarity 63.0% nes 58; Conservative
  10-MAR-2005 (first entry)
  Li M;
  WPI; 2004-099606/11.
   P-PSDB; ADW14378
   Chen C, Xiu C,
   Homo sapiens
  CN1424325-A.
  ADW14377;
  62
  Query Match
  Best Loca
Matches
   RESULT 7
ADW14377
     SKGGG
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   This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide with may be produced using the expression cassette of the invention.
  The invention comprises an expression cassette which produces a tandem polyypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an
   61
  61
  2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   2 CUGUNUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
   Gaps
                                  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   ö
   ch 74.8%; Score 69.6; DB 12; Length 102; 1 Similarity 63.0%; Pred. No. 1.9e-14; 58; Conservative 20; Mismatches 14; Indels 0.
   expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
  Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;
   UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   Disclosure; SEQ ID NO 33; 132pp; English.
  Disclosure, SEQ ID NO 60; 157pp; English.
   PTH peptide coding sequence #1
  ADJ65857 standard; DNA; 102 BP
  24-MAY-2002; 2002US-0383212P.
  23-MAY-2003; 2003WO-US016645.
   (first entry)
   (REST-) RESTORAGEN INC
   WPI; 2004-035129/03.
P-PSDB; ADJ65837.
     P-PSDB; ADG93159
   WO2003100022-A2
   Peng L;
   Unidentified
   06-MAY-2004
   04-DEC-2003
  62
  ADJ65857;
  ery Match
   Xia Y,
   Matches
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ADG93180 RESULT

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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
  2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  2 CUGUIUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
  ds; parathyroxin; recombinant protein; protein engineering
expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
   Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
  74.8%; Score 69.6; DB 12; 63.0%; Pred. No. 1.9e-14; ive 20; Mismatches 14;
  (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  ::||||:|||:|||:|||:||||||||::
TTGAATGGCTGCGTAAAAACTGCAGGACGTT
   Disclosure; SEQ ID NO 34; 132pp; English.
   12-DEC-2001; 2001CN-00142627.
   24-MAY-2002; 2002US-0383212P.
  12-DEC-2001; 2001CN-00142627
  23-MAY-2003; 2003WO-US016645.
   ADW14375 standard; DNA; 111
   (first entry)
  Local Similarity 63.09
nes 58; Conservative
   (REST-) RESTORAGEN INC
   WPI; 2004-035129/03.
  P-PSDB; ADJ65838
  WO2003100022-A2
  Peng L;
   Homo sapiens
   10-MAR-2005
  CN1424325-A.
   18-JUN-2003
   04-DEC-2003
  ADW14375;
  Query Match
  Xia Y,
  Best Loca
Matches
  RESULT 10
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   This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nuclaic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
   2 cugutuccaaauccaacucaugcacaguaguaguaguaguagucugaacuccauggaacgug 61
   Gaps
  Novel expression cassette-related polypeptide-encoding DNA SeqID61.
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   ö
  74.8%; Score 69.6; DB 12; Length 111; 63.0%; Pred. No. 1.9e-14; ive 20; Mismatches 14; Indels 0
   expression cassette; high yield polypeptide production;
tandem polypeptide; inclusion body; gene; ds.
  Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
   UNGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  Disclosure; SEQ ID NO 61; 157pp; English.
  Xia Y;
  Luan P,
  PTH peptide coding sequence #2.
   ADG93180 standard; DNA; 111 BP.
   23-MAY-2003; 2003WO-US016643.
  24-MAY-2002; 2002US-0383370P
   ADJ65858 standard; DNA; 111
   (first entry)
  Query Match
Best Local Similarity 63.04
Matches 58; Conservative
   (first entry)
  Harley S, Williams JA,
   (REST-) RESTORAGEN INC
   WPI; 2004-035128/03.
P-PSDB; ADG93160.
   HARLEY S.
   WO2003100021-A2
   11-MAR-2004
  Unidentified
  04-DEC-2003
  62
  ADG93180
  ADJ65858
   (HARL/)
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Indels

93

ADJ65858 XX XX AC ADJ6 XX DT 06-M XX

RESULT 9

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Length 111;

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RESULT 12
AAT34865
 SSSSSSSS
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   This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed
  The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PrH 1-34 peptide (ADWH4376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADWH4378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the Gly-Ser-Pro-PTH 1-34 peptide.
   2 cugunoccapanoccaccucanoccaccuceuceuceuceuceuceuceacuccauceaaceuc 61
   Gaps
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  Production of reorganized human parathyroid hormone 1-34 peptide
   .;
0
  Match 74.8%; Score 69.6; DB 13; Length 111; Local Similarity 63.0%; Pred. No. 1.9e-14; les 58; Conservative 20; Mismatches 14; Indels 0;
  expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body; gene; ds; PTH.
   Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;
   Novel expression cassette-related PTH DNA SeqID141.
   ::|||:|||:|||:|||:||||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  Disclosure; SEQ ID NO 141; 157pp; English.
   Xia Y;
  Claim 3; SEQ ID NO 1; 25pp; Chinese.
   Luan P,
  BP
  23-MAY-2003; 2003WO-US016643
  24-MAY-2002; 2002US-0383370P
   ADG93260 standard; DNA; 117
   (first entry)
  Harley S, Williams JA,
   (REST-) RESTORAGEN INC. (HARL/) HARLEY S.
  WPI; 2004-035128/03.
P-PSDB; ADG93259.
Ľį
                    WPI; 2004-099606/11.
                               P-PSDB; ADW14376
 Xiu C,
   WO2003100021-A2
   Unidentified.
   11-MAR-2004
   04-DEC-2003
  Synthetic.
  ADG93260;
   Query Match
 Chen C,
   Matches
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   PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide; alpha-carboxamide; recombinant protein; fusion protein; transpeptidation; vector; plasmid pBN1; carbonic anhydrase II; ss.
   61
in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a PTH peptide which was used in the exemplification of the invention.
  2 CTGTTTCTGAAATCCAGCTGATGCACACCTGGGTAAACACCTGAACTCTATGGAACGTG 61
  A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding for a fusion protein (AAR87867) composed of the C-terminal end of human carbonic anhydrase II joined by an intraconnecting peptide (including a thrombin cleavage site) to amino acids 1-34 of PTH (AAR8866), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in E. coli transformants. The intraconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be selectively reacted to produce C-terminal carboxamidated PTH(1-34)
  Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage and transpeptidation of recombinant multicopy peptide(s) or fusion
   2 cuguruccaaauccaacucauccacegueguegueguegucucaacuccauegaaccuc
   0; Gaps
   Heriksen DB, Holmquist B, Wagner FW;
   Length 117;
   "hCA-linker-PTH(1-34)Cys fusion"
  Plasmid pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
   Indels
   Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;
   Seguence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;
  Query Match 74.8%; Score 69.6; DB 12; Best Local Similarity 63.0%; Pred. No. 1.9e-14; Matches 58; Conservative 20; Mismatches 14;
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
  Location/Qualifiers
  Example 7; Fig 1; 93pp; English.
  AAT34865 standard; cDNA; 168 BP.
   94US-00350528.
   95WO-US015799
   1. .162
/*tag= a
/product= "
  02-DEC-1996 (first entry)
   Stout JS, Patridge BE,
   (BION-) BIONEBRASKA INC
   WPI; 1996-287185/29.
  P-PSDB; AAR98967.
   07-DEC-1995;
   07-DEC-1994;
   WO9617941-A2
   13-JUN-1996.
  constructs
  Synthetic.
  AAT34865;
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7

Matches

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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a protein which may be used in the construction of a tandem polypeptide
   CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUCCCAGAACGUG
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  expression cassette; tandem polypeptide; inclusion body;
   expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
  Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
   Tandem polypeptide-encoding expression cassette #6
  74.8%; Score 69.6; DB 12; 63.0%; Pred. No. 2.4e-14; ive 20; Mismatches 14;
   TGAATGGCTGCGTAAAAACTGCAGGACGTT 93
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
62 TIGAATGGCTGCGTAAAAAACTGCAGGACGIT 93
   Disclosure; SEQ ID NO 35; 132pp; English.
   BB
  ВР
   23-MAY-2003; 2003WO-US016645
  24-MAY-2002; 2002US-0383212P
   ADJ65859 standard; DNA; 252
  PTH protein coding sequence
  ADJ65913 standard; DNA; 264
  (first entry)
   (first entry)
  58; Conservative
   (REST-) RESTORAGEN INC.
   WPI; 2004-035129/03.
   Query Match
Best Local Similarity
   of the invention.
  P-PSDB; ADJ65839
   WO2003100022-A2.
  Peng L;
  Unidentified.
   06-MAY-2004
  06-MAY-2004
  04-DEC-2003
   ~
  62
   ADJ65913;
  ADJ65859;
  xia Y,
   Best Loc
Matches
   RESULT 15
  RESULT 14
ADJ65859
  ADJ65913
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  This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
  2 CUGUIUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG 61
   61
   61
  2 CTGITICTGAAATCCAGCTGATGCACAACCTGGGTAAACACCCTGAACTTGT
   CUGUIUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCGUCUGAACUCCAUGGAACGUG
  Gaps
   Gaps
   Novel expression cassette-related polypeptide-encoding DNA SeqID62
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  ;
0
   ö
  74.8%; Score 69.6; DB 12; Length 252; 63.0%; Pred. No. 2.4e-14; Indels 0; ive 20; Mismatches 14; Indels 0;
                     Length 168;
  14; Indels
  expression cassette; high yield polypeptide production;
tandem polypeptide; inclusion body; gene; ds.
   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
                       DB 2;
                     ; Score 69.6; DB 2;
; Pred. No. 2.1e-14;
20; Mismatches 14
  ::|||:||:|||:|||:|||||||||::
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93 ::|||:|||:|||:|||::
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   Disclosure; SEQ ID NO 62; 157pp; English.
  ;
  Xia
  ٦,
   ADG93181 standard; DNA; 252 BP.
  Luan
   23-MAY-2003; 2003WO-US016643.
  24-MAY-2002; 2002US-0383370P.
                       74.8%;
  (first entry)
  Local Similarity 63.0
nes 58; Conservative
  58; Conservative
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  11-MAR-2004
  04-DEC-2003.
  Harley S,
  ADG93181;
  47
  Query Match
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Gaps

; 0

Length 252; Indels 61

Matches

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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence represents an expression cassette which encodes a tandem polypeptide of the invention.
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  Query Match
74.8%; Score 69.6; DB 12; Length 264;
Best Local Similarity 63.0%; Pred. No. 2.4e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0;
  Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;
  Disclosure; SEQ ID NO 89; 132pp; English.
inclusion body fusion partner; gene; ds.
   24-MAY-2002; 2002US-0383212P.
  23-MAY-2003; 2003WO-US016645.
   (REST-) RESTORAGEN INC.
  WPI; 2004-035129/03.
P-PSDB; ADJ65912.
   WO2003100022-A2.
  Xia Y, Peng L;
                                 Unidentified
  04-DEC-2003.
```

; 0

0; Gaps

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62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:|||||:: 65 TIGAATGGCTGCGTAAAAAACTGCAGGACGTT 96

Search completed: November 23, 2005, 23:00:14 Job time : 244.667 secs

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November 23, 2005, 22:35:17; Search time 1177.67 Seconds (without alignments) 4488.911 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
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  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM nucleic - nucleic search, using sw model
  IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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93
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2: 9b_pat:*
9b_pat:*
9b_pi:*
  gb_un: *
gb_un: *
gb_vi: *
gb_htg: *
gb_pl: *
  10:
  Title:
Perfect score:
Sequence:
  Scoring table:
  Database :
   Searched:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |   | Description              |          | _        | BD266834 PTH funct | AR269042 Sequence | AR005132 Sequence | AR005133 Sequence | AR177779 Sequence | AR177780 Sequence |          | BD234383 Recombina | BD234385 Recombina | BD234386 Recombina | BD234384 Recombina | BD234390 Recombina | BD234387 Recombina | BD234388 Recombina | BD234389 Recombina | A36847 Sequence 1 |
|-----------|---|--------------------------|----------|----------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| SUMMARIES |   | ΩI                       | BD266832 | BD266833 | BD266834           | AR269042          | AR005132          | AR005133          | AR177779          | AR177780          | AR043797 | BD234383           | BD234385           | BD234386           | BD234384           | BD234390           | BD234387           | BD234388           | BD234389           | A36847            |
|           |   | DB                       | 9        | 9        | 9                  | ø                 | 9                 | 9                 | 9                 | 9                 | 9        | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                 |
|           |   | Query<br>Match Length DB | 93       | 93       | 93                 | 258               | 141               | 141               | 141               | 141               | 207      | 405                | 408                | 408                | 411                | 414                | 417                | 423                | 435                | 717               |
|           | æ | Query<br>Match           | 100.0    | 89.7     | 79.4               | 71.4              | 68.6              | 9.89              | 68.6              | 68.6              | 9.89     | 64.5               | 64.5               | 64.5               | 64.5               | 64.5               | 64.5               | 64.5               | 64.5               | 61.7              |
|           |   | Score                    | 93       | 83.4     | 73.8               | 66.4              | 63.8              | 63.8              | 63.8              | 63.8              | 63.8     | 09                 | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 57.4              |
|           |   | Result<br>No.            | 7        | 7        | m                  | 4                 | ഗ                 | 9                 | 7                 | υ<br>Θ            | 6        | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                |

|                                                                | AR030635 Sequence AR168173 Sequence E05658 DNA encodin E05673 DNA encodin I83594 Sequence 1 AR0272020 Sequence EAR027205 Sequence | E04535 Syntheric D<br>E05671 DNA encodin<br>183595 Sequence 3<br>871759 human parat<br>AR027021 Sequence<br>E05672 DNA encodin<br>183596 Sequence 4<br>BDJ70195 Process f | BD170212 FOCCESS I<br>BD170213 Process f<br>BD17019 Process f<br>AR027050 Sequence<br>BD170196 Process f<br>E05677 DNA encodin<br>BD140917 Process f                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|----------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 6 A36849<br>6 AR027046<br>6 E05675<br>6 AR027011<br>6 AR027044 | 6 AR030635<br>6 AR168173<br>6 E05658<br>6 E05673<br>6 I83594<br>6 AR027020                                                        | H                                                                                                                                                                         | 6 BD170222<br>6 BD170213<br>6 BD170213<br>6 BD170198<br>6 AR027050<br>6 BD170196<br>6 E05677<br>6 BD140917                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ~ ~ ~ 10.10                                                    | 6.6<br>6.6<br>6.6<br>6.6<br>6.6<br>6.6<br>7.6<br>7.6<br>7.6<br>7.6                                                                |                                                                                                                                                                           | 54.8 186<br>54.8 201<br>54.8 225<br>54.8 252<br>54.8 252<br>54.8 252                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| 19<br>20<br>22<br>23                                           | 2 2 2 2 2 4 8 2 2 4 8 2 2 2 2 2 2 2 2 2                                                                                           | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                     | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

## ALIGNMENTS

| RESULT 1   |                                                                                   |
|------------|-----------------------------------------------------------------------------------|
| BD266832   |                                                                                   |
| rocus      | linear PAT 17-JU                                                                  |
| DEFINITION | PTH functional domain conjugate peptides, derivatives thereof and                 |
|            | novel tethered ligand-receptor molecules.                                         |
| ACCESSION  |                                                                                   |
| VERSION    | BD266832.1 GI:33076600                                                            |
| KEYWORDS   | JP 2002533115-A/1.                                                                |
| SOURCE     | synthetic construct                                                               |
| ORGANISM   | synthetic construct                                                               |
|            | other sequences; artificial sequences.                                            |
| REFERENCE  |                                                                                   |
| AUTHORS    | and Jueppner, H.                                                                  |
| TITLE      | PTH functional domain conjugate peptides, derivatives thereof and                 |
|            | novel tethered ligand-receptor molecules                                          |
| JOURNAL    | Patent: JP 2002533115-A 1 08-OCT-2002;                                            |
|            | THE GENERAL HOSPITAL CORP                                                         |
| COMMENT    | OS Artificial Sequence                                                            |
|            | PN JP 2002533115-A/1                                                              |
|            | PD 08-OCT-2002                                                                    |
|            | 30-DEC-1999 JP 20(                                                                |
|            | 31-DEC-1998 US 60/114577                                                          |
|            | THOMAS J GARDELLA,                                                                |
|            | JUEPPINER                                                                         |
|            | <pre>pC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC</pre> |
|            | A61P19/10,                                                                        |
|            | PC A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC            |
|            | C12N1/21,                                                                         |
|            | 10, G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02                          |
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100.0%; Score 93; DB 6; Length 93;

Query Match

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

LOCUS

RESULT 2 BD266833

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synthetic construct
synthetic construct
construct
synthetic construct
cother sequences; artificial sequences.

I (bases 1 to 93)
S dardella_T.7. Kronenberg,H.M., Potts,J.T. and Jueppner,H.
Gardella_T.0. Kronenberg,H.M., Potts,J.T. and Jueppner,H.
PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

L Patent: JP 2002533115-A 3 08-OCT-2002;
THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002533115-A/3
PD 08-OCT-2002
PR 31-DEC-1999 US 060/21171
PR 31-DEC-1999 US 060/214577
PI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD PI
   CIZNIS/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC A61P19/10,
  A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC
   linear PAT 10-APR-2003
   C12N1/21,
PC C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N5/10, A61K37/02 CC
Description of Artificial Sequence: modified PTH sequence FH Key
Location/Qualifiers
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  Unknown.

Unclassified.

1 (Bases 1 to 258)

Jung, E.-K., Park, D.-H. and Chung, S.-I.

Recombinant expression vector of human parathyroid hormone

Patent: US 6500647-A 26 31-DEC-2002;

Mogam Biotechnology Research Institute; Kyonggi-Do;

KRX;
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  258 bp I Sequence 26 from patent US 6500647. AR269042

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  Location/Qualifiers
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ORGANISM
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   DEFINITION
  REFERENCE
AUTHORS
TITLE
  AUTHORS
TITLE
JOURNAL
   ACCESSION
VERSION
KEYWORDS
  JOURNAL
   REFERENCE
   RESULT 4
AR269042
   FEATURES
  FEATURES
  COMMENT
   ORIGIN
  ORIGIN
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  g
   BD266833.1 GI:33076601
BD266833.1 GI:33076601
BD266833.1 GI:33076601

SP 2002533115-A/2.

Synthetic construct
construct
to ther sequences, artificial sequences.

The requences, artificial sequences.

Gardella.T.J. Kronenberg.H.M., Potts,J.T. and Jueppner,H.

FIH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

Artificial Sequence

OS Artificial Sequence
PD 08-CT-2002;

PP 31-DEC-1999 US 2000591171

PR 31-DEC-1999 US 60/114577

FI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD PI
   PTH functional domain conjugate peptides, derivatives thereof and movel tethered ligand-receptor molecules. BD266834 BD266834.1 GI:33076602
   93 bp RNA linear PAT 17-JUL-2003
PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
   L2N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC
  A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC
   C12N1/21,
PC C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02 CC
Description of Artificial Sequence: modified PTH sequence FH Key
Location/Qualifiers
   1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
   1 GCUGUIUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
   1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTGGTGGTTCCATGGAACGT
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                              Gaps
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   ice 1. .93
/organism='Artificial Sequence'.
Location/Qualifiers
   / Match 89.7%; Score 83.4; DB 6; Length 93; Local Similarity 68.8%; Pred. No. 2.6e-17; Nes 64; Conservative 23; Mismatches 6; Indels
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Method for increasing the electrotransport
Patent: US 5747453-A 5 05-MAY-1998;
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Method for increasing the electrotransport flux of polypeptides
Patent: US 6313092-A 3 06-NOV-2001;
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Holladay,L.A. and Oldenburg,K.R.
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21 (bases 1 to 408)

22 (bases 1 to 408)

23 Alale, JE., Hershberger, C.L., Larson, J.L. and Menke, M.A.

24 Recombinant synthesis of beta-lipotropin and other peptides

25 Patent: JP 2002533072-A 6 08-OCT-2002;

26 ELI LILLY AND CO

27 OS Artificial Sequence

28 PN 2002533072-A/6

29 D8-OCT-2002

29 PP 15-DEC-1999 JP 2000589671

20 PR 21-DEC-1999 US 60/113058

20 PR 21-DEC-1999 US 60/113058

20 PR 21-DEC-1999 US 60/113058

21 OHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,

27 PI MICHAEL ANDREW MERKE

28 PC C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21 PC

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28 C12P21/02, C12N15/00

29 C12P21/02, C12N15/00

20 Description of Artificial Sequence: PCpB-IEGR-hPTH fusion FH

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ET CDS C1CPTICALON STATEMENT CONTRIBITIES

ET CDS C1CPTICALON STATEMENT CONTRIBITIES

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RS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

RS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

Recombinant synthesis of beta-lipotropin and other peptides

Patent: JP 2002533072-A 5 08-OCT-2002;

ELI LILLY AND CO

OS Artificial Sequence

PN 9P 2002533072-A/5

PD 08-OCT-2002

PF 15-DEC-1999 UP 2000589671

PR 15-DEC-1999 US 60/113058

PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,

PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,

PC C12N15/09, COTX14/67, CO7K19/00, C12N1/15, C12N1/19, C12N1/21 PC

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18 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

18 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

19 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

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15 Hale, J.E., Hershberger, J.L. and Menke, M.A.

16 Hale, J.E., Hershberger, J.L. and Menke, M.A.

16 Hale, J.E., Hershberger, J.L. and Menke, M.A.

17 Hale, J.E., Hershberger, J.L. and Menke, M.A.

18 Hale, J.L. and Menke, M.
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Hale, J.E., Hershberger, C.L., Larson, J.L. and Recombinant synthesis of beta-lipotropin and Patent: JP 2002533072-A 11 08-OCT-2002;

ELI LILLY AND CO
OS Artificial Sequence
PN JP 2002533072-A/11

PD 08-OCT-2002

PF 15-DEC-1999 JP 2000589671

PR 21-DEC-1998 US 60/113058

PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGI
PI MICHAEL ANDREW MENKE
PC C12N15/09, CO7K14/67, CO7K19/00, C12N1/15

PC C12N5/10, C12N15/00, C12N5/00

PC C12P21/02, C1N15/00, C12N5/00

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   302 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 361
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   synthetic construct synthetic construct
   synthetic construct synthetic construct other sequences; artificial sequences.
  2 cugurucceaaauccaecucauecaceuceuceuceuceucucaacuccauecaaceuc 61
   Similarity
53; Conserv
  other sequences; artificial sequences
  BD234390.1 GI:33044160 JP 2002533072-A/11.
   JP 2002533072-A/8.
   BD234387.1 GI:33044157
   BD234387
  Recombinant synthesis of
   BD234387
   15-DEC-1999 JP 2000589671
21-DEC-1998 US 60/113058
JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON, MICHAEL ANDREW MENKE
C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
   64.5%;
ilarity 57.6%;
Conservative 1
  C12P21/02.C12N15/00,C12N5/00
C12P21/02.C12N15/00,C12N5/00
Description of Artificial Sequence: PCpB-APR-hPTH fusion FH
Location/Qualifiers
CDS (4). . (402).
  15-DEC-1999 JP 2000589671
21-DEC-1998 US 60/113058
JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON, MICHAEL ANDREW MENKE
C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21 PC
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Pred. No. 2.5e-09;
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  417 bp DNA linear PAT 17-J
beta-lipotropin and other peptides.
   Length 414;
   and
   Indels
  Menke, M.A.
other peptides
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  Gaps
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Result
No.
  Run on:
  OM nucleic - nucleic search, using sw
  Database
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
  Total number of hits satisfying chosen parameters:
   Scoring table:
  Sequence:
  Perfect score:
   Title:
  ი
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
November 23, 2005, 22:36:53 ; Search time 1823 Seconds (without alignments) 2386.834 Million cell updates/sec
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Match
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Gapop 10.0 , Gapext 1.0
  US-09-475-158A-14
93
   41078325 seqs, 23393541228 residues
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  EST: *
  gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
   gb_gss1: *
gb_gss2: *
gb_gss3: *
  gb_est4:*
gb_est5:*
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gb_est7:*
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gb_est2:*
gb_est3:*
  Length
  띪
W19763
W3966
W39708
W31998
W31998
W319764
W56235
W31077
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W19765
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W3966 zb34c06.r1
W3966 zb34c06.r1
W37708 zc10d12.r1
W31798 zb96d06.r1
W31998 zb96d06.r1
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W39102 zb35h03.r1
BG19854 RST17829
AI05197 cy29c05.x
BX106232 BX106232
BG188276 RST7729
AX372113 EST83988 Hu
W529548 EST83988 Hu
W529548 EST83988 Hu
  Description
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |          |          |          |          |          |          |          |             |          |          |          |          |          |          |            |          |          |          |          |          |          |          | ი        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|----------|----------|----------|----------|----------|----------|-------------|----------|----------|----------|----------|----------|----------|------------|----------|----------|----------|----------|----------|----------|----------|----------|
| . 2 49.7 766 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 45       | 44       | 43       | 42       | 41       | 40       | 39       | 3<br>8<br>8 | 37       | 36       | ω<br>5   | 34       | ω<br>ω   | 32       | <u>3</u> 1 | 30       | 29       | 28       | 27       | 26       | 25       | 24       | 23       |
| 9.7 766 L AA843141 4.5 398 B DN347669 4.5 431 8 DN348158 4.5 431 8 DN347054 4.5 432 8 DN347054 4.5 447 8 DN347669 4.5 447 8 DN34783 4.5 451 8 DN347334 4.5 451 8 DN347334 4.5 452 8 DN347142 4.5 502 8 DN347142 4.5 507 8 DN348158 4.5 508 B DN34817 4.5 523 8 DN34817 4.5 528 8 DN348165 4.5 528 8 DN348165 4.5 531 8 DN348165 4.5 531 8 DN348165 4.5 531 8 DN348165 4.5 531 8 DN348165 4.5 533 8 DN348165 | 41.4     | 41.4     | 41.4     | 41.4     | 41.4     | 41.4     | 41.4     | 41.4        | 41.4     | 41.4     | 41.4     | 41.4     | 41.4     | 41.4     | 41.4       | 41.4     | •        | •        | •        | •        | •        | •        | 46.2     |
| B DN347669 B DN348158 B DN347958 B DN3479054 B DN3479054 B DN3479081 B DN3477081 B DN3477334 B DN3477146 B DN3477146 B DN3477146 B DN3477146 B DN3477146 B DN347706 B DN347706 B DN348558 B DN348565 B DN348656                                                                                | 44.5     | •        | •        | •        | •        | •        | •        | 44.5        | 44.5     | 44.5     | 44.5     | 44.5     | 44.5     | 44.5     | 44.5       | 44.5     | 44.5     |          |          | 4        | 4        | 4        | 9        |
| AA843141 DN347669 DN348158 DN349208 DN349208 DN347064 DN346969 DN347081 DN347334 DN347334 DN347334 DN347142 DN347146 DN347234 DN347165 DN348166 DN348165 DN348165 DN348165 DN348165 DN34834816                                                                                                                                                                                                                                                                                                                                                   | 543      | 542      | 540      | 533      | 531      | 528      | 528      | 523         | 518      | 507      | 502      | 462      | 459      | 458      | 451        | 451      | 447      | 442      | 439      | 431      | 413      | 398      | 766      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | œ        | œ        | œ        | œ        | œ        | œ        | œ        | œ           | œ        | œ        | œ        | œ        | œ        | œ        | œ          | œ        | œ        | 8        | æ        | æ        | œ        | œ        | ۲        |
| DN34769<br>DN34769<br>DN3479208<br>DN349208<br>DN346969<br>DN346969<br>DN346969<br>DN3467133<br>DN347133<br>DN347133<br>DN347142<br>DN347146<br>DN347146<br>DN3487165<br>DN348145<br>DN348145<br>DN348145<br>DN348145<br>DN348145<br>DN348165<br>DN348165<br>DN348165<br>DN348165<br>DN348165<br>DN348165<br>DN348165                                                                                                                                                                                                                            | DN348441 | DN348349 | DN348316 | DN347653 | DN348165 | DN348145 | DN347706 | DN348206    | DN348137 | DN350926 | DN348558 | DN347146 | DN347234 | DN347142 | DN347334   | DN346863 | DN347081 | DN346969 | DN347054 | DN349208 | DN348158 | DN347669 | AAB43141 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | DN34844  | DN34834  | DN348316 | DN347653 | DN348165 | DN348145 | DN347706 | DN348206    | DN348137 | DN350926 | DN348558 | DN347146 | DN347234 | DN347142 | DN347334   | DN346863 | DN347081 | DN346969 | DN347054 | DN349208 | DN348158 | DN347669 | 1110000  |

## ALIGNMENTS

|                                                                                                                                                                                                                                                                                                                                                                                                               | FEATURES<br>source                                                                                                                                |                                                                                                                                                                                         | TITLE<br>JOURNAL<br>COMMENT                                                                                                                                                                      | REFERENCE<br>AUTHORS                                                                                                                                                                                                                                                                                                  | ACCESSION VERSION KEYWORDS SOURCE ORGANISM                                                                                                                  | RESULT 1 W19763 LOCUS DEFINITION                                                                                                                                                |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
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AI031553 ow48c08.x

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Query Match
  120
  Tel: 314 286 1800
Fax: 314 286 1800
Email: estiwation wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: mob.REGA+ET
Seg quality sequence stor.
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
: |||:||:||:|| || |:|||||| |:
|20 TAGAATGGCTGCGTAAGAANCTGCAGGATGT 150
  60
   Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
   Hominidae, Homo.

(bases 1 to 352)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Clark, N., Kucaba, T., Le, M., Lennon, G., Marra, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Aifkin, L., Rohlfing, T., Soares, M., Tan, F., Tarvaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
   352 bp mRNA linear EST 15-MAY-1996 zb34c06.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
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  49;
  The WashU-Merck EST Project Unpublished (1995)
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  Similarity
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   Score 48.4; DB 8;
Pred. No. 2.9e-05;
5; Mismatches 27;
   Length 324;
  61
  0
   RESULT
W38966
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  ORIGIN
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RESULT 2 W39062 LOCUS DEFINITION

ACCESSION VERSION

KEYWORDS ORGANISM

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Local

JOURNAL COMMENT

FEATURES

source

REFERENCE AUTHORS

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Institute
NIH."
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TITLE
JOURNAL
COMMENT
  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   REFERENCE
AUTHORS
  FEATURES
  DEFINITION
   Query Match
Best Local S
Matches 49
  source
  245
  185
   62
  49;
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: mob.REGA+ET.
  The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Fax: 314 286 1810
  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M. Parsons, J., Rikkin, L., Rohlfing, T., Soarres, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
   Homo sapiens (human)
Homo sapiens
   W38966

Zb28bl2:1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN); mRNA sequence.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   W38966.1 GI:1320674
   Hominidae; Homo.
  Similarity
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/note="Organ: parathyroid_gland; Vector: pT7T3D
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Site_2: Eco RI; 1st strand cDNA was primed with
location/Qualifiers
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  Score 47.8; DB 8;
Pred. No. 4.7e-05;
5; Mismatches 27;
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   Length
  8
   information.
  Marra,M.,
  0
                                    Not I;
a Not I -
  244
   61
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RESULT 4
W37708
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  밁
  COMMENT
   REFERENCE
  SOURCE
ORGANISM
  KEYWORDS
  DEFINITION
  FEATURES
   VERSION
   ACCESSION
   TITLE
JOURNAL
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  AUTHORS
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  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
  49;
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   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
   Unpublished (1995)
   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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  The WashU-Merck EST Project
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314 286 1810
   quality sequence stop: 396.
Location/Qualifiers
  sapiens (human)
  Conservative
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                                    /lab_host="DH108" (ampicillin resistant)"
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/clone="Organ: parathyroid gland, VecTor: pT7T3D
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  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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   Length 376;
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   MO 63108
   G., Marra, M.,
   EST 10-OCT-1996
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PUBMED
COMMENT
  VERSION
KEYWORDS
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  REFERENCE
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   DEFINITION
   TITLE
JOURNAL
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  Query Match
   AUTHORS
   ORGANISM
   Local
   270 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
  Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Kucaba, T., Lacy, M., Le, M., Le, N., Hultman, M., Kucaba, T., Lacy, M., Prange, C., Rifkin, L., Mardis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
  49;
  W31998 416 bp mRNA linear EST 20-AUG-1999 zb96d06.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   8889549
Contact: Wilson RK
   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
  Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homo sapiens
  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 771 Std Error: 0.00
   Tel: 314 286 1800 Fax: 314 286 1810
   Washington University School of Medicine
   Hominidae; Homo.
1 (bases 1 to 416)
   W31998.1 GI:1313010
   W31998
   Seq primer: mob.REGA+ET
  Email: est@watson.wustl.edu
  Homo sapiens (human)
  (HUMAN);, mRNA sequence.
  Similarity
  CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
  quality sequence
  Conservative
  TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
/clone lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
(pharmacia) with a modified polylinker; Site_1:
  /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
   mol_type="mRNA"
  organism="Homo sapiens"
   ocation/Qualifiers
   'db_xref="taxon:9606"
'clone="IMAGE:320651"
  db_xref="GDB:1258309"
   .416
   51.4%;
  15;
   Std Error: 0.00
  Score 47.8; DB 8;
Pred. No. 4.8e-05;
  stop: 386.
  Mismatches
   92
  Louis,
   Length 411;
   linear
  3
   EST 20-AUG-1996
   0
  269
   61
   0
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Not

SOURCE

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ORIGIN

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W31998

RESULT

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ACCESSION
VERSION
KEYWORDS
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JOURNAL
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   Local
   Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
  94
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   49;
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High
  Hominidae; Homo.

1 (bases 1 to 434)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Alfkin,L., Rohlfing,T., Soarses,M., Tan,F.,
Parsons,J., Alfkin,L., Rohlfing,T., Soarses,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  W38764: 13-MAY-1996 TENAN Linear EST 15-MAY-1996 TED27807: 1 Soares parathyroid tumor NbHPA Homo sapiens CDNA Clone IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN); mRNA sequence.
  The WashU-Merck EST Project Unpublished (1995)
   Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
   W38764
W38764.1 GI:1320471
   Similarity
  TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 124
   CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG
  primer: mob.REGA+ET
n quality sequence stop: 253.
Location/Qualifiers
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/dev stage="adult"
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/clone_lib="Soares_parathyroid_tumor_NbHPA"
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Site_2: Eco RI; 1st strand cDNA was primed with a Not
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  /mol_type="mRNA"
/db_xref="GDB:1248198"
  organism="Homo sapiens"
  51.4%; Score 47.8; DB 8; 53.8%; Pred. No. 4.8e-05; rive 15; Mismatches 27;
   Length 416;
   0
   93
   61
   0
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REFERENCE AUTHORS

COMMENT

FEATURES

oligo(dT) primer

. a Not Not I RESULT W38764

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```
Query Match
Best Local
    49;
                          Similarity
       Conservative
   TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
  51.4%;
    15;
Score 47.8; DB 8;
Pred. No. 4.8e-05;
5; Mismatches 27;
   Length 434;
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       0
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ORIGIN

TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT W56235 밁 Ś 밁 Ş FEATURES DEFINITION Matches source 174 Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 865 Std Error: 0.00
Seq primer: mob.REGA+ET. The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, Hominidae, Homo.

(bases 1 to 450)

1 (bases 1 to 450)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Holman, M., Hultman, M., Kucaba, T., Loares, M., Tan, F., Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and W56235
zc01e11.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:321068 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens (human) (HUMAN);, mRNA sequence. : |||:|||:|| || || ||:|| || : || || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || cugurucceaaauccaecueauecaceueeueeueeucceuccaaecaceuc /tissue\_type="parathyroid tumor"
/dev stage="adult"
/lab host="DH10B (ampicillin resistant)"
/clone\_lib="Soares\_parathyroid\_tumor\_NbHPA"
/note="Organ: parathyroid\_gland; VecTor: pT7T3D
/pharmacia) with a modified polylinker; Site 1:
Site\_2: Eco RI; 1st strand cDNA was primed with /organism="Homo sapiens"
/mol\_type="mRNA"
/db\_xref="GDB:1258726" Location/Qualifiers /db\_xref="taxon:9606" /clone="IMAGE:321068" Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Euarchontoglires; Primates; Catarrhini; **™** Marra, M., 61

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ACCESSION
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Matches
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  AUTHORS
  ORGANISM
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  Local Similarity
  249
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  49;
  N
  W33077
453 bp mRNA linear EST 10-OCT-1990 zc07a12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 871 Std Error: 0.00
  The WashU-Merck EST Project Unpublished (1995)
   Hominidae; Homo.

1 (bases 1 to 453)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  W33077.1 GI:1315062
  Insert Length: 871
  Contact: Wilson RK
  Homo sapiens
  Homo sapiens (human)
   HUMAN);, mRNA sequence.
  TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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/db_xref="taxon:9606"
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              /clone lib="Soares parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: pT7T3D
/Pharmacia) with a modified polylinker; Site 1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not
  /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
   51.4%;
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Pred. No. 4.9e-05;
L5; Mismatches 27;
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  Indels
   EST 10-OCT-1996
   Marra, M.,
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  Gaps
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```

FEATURES

COMMENT

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```
Query Match
  Local Similarity
  201
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU
   49;
  2 cugurucceananuccaecueanecaecueaueaueaueaueaucueanecaecaneeaaceue 61
  W56820
496 bp mRNA linear EST 10-OCT zc01a03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA cl mAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECU
   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 858 Std Error: 0.00
  Tel: 314 286 1800
Fax: 314 286 1810
  Contact: Wilson RK Washington University School of Medicine
   1 (bases 1 to 496)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   Homo sapiens
   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  The WashU-Merck EST Project
   Hominidae; Homo.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Homo sapiens (human)
  W56820.1 GI:1358743
   Seq primer: mob.REGA+ET
  Unpublished (1995)
  Wilson, R
   (HUMAN);, mRNA sequence.
  TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 291
  quality sequence stop: 424.
   Conservative
  TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
   /clone lib="Soares parathyroid tumor NbHPA"
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Site 2: Eco RI; 1st strand cDNA was primed with
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/lab_host="DH10B (ampicillin resistant)"
   /mol_type="mRNA"
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/db_xref="taxon:9606"
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  location/Qualifiers
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Pred. No. 4.9e-05;
5; Mismatches 27;
   Length 453;
   Indels
  Marra, M.,
  EST 10-OCT-1996
   <u>.</u>
          Not I
  PRECURSOR
   Gaps
  260
  0
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ACCESSION VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

W56820 LOCUS

RESULT

DEFINITION

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Matches

ORIGIN

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TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
  FEATURES
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AUTHORS
  ORGANISM
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W19765
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   239
   179
  62
  1 Similarity 53.4
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@simage.llnl.gov) for further information.
Seq_primer: mob.REGA+ET
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
  #19765

zb39c03.rl Soares parathyroid tumor NDHPA Homo sapiens cDNA clone IMAGE:305956 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
   2 cugurucceaaauccaecueauecaceueeueeueeueucueaacuccaueeaaceue
   Unpublished (1995)
Contact: Wilson RK
  The WashU-Merck EST Project 
Unpublished (1995)
  Hominidae, Homo.

1 (bases 1 to 536)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   W19765
W19765.1 GI:1295882
EST.
  Homo sapiens (human)
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
  TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 269
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   314 286 1800
314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pT713D
/note="Organ: parathyroid gland; Vector: pT713D
/Pharmacia) with a modified polylinker; Site_1:
Site_2: Eco RI; 1st strand cDNA was primed with
oligo(dT) primer
   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
  clone="IMAGE:305956"
                   igo(dT)
go(dT) primer
-TGTTACCAATCTGAAGIGGGAGCGGCCGCACCAAFTTTTTTTTTTTTTTTTTTTT
   51.4%;
  15;
  Score 47.8; DB Pred. No. 5e-05; Mismatches
  27;
  8
  Length
  Indels
  496;
   Marra, M.,
  0
  þ
  Not I;
a Not I -
   238
   61
  0
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COMMENT

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VERSION
KEYWORDS
  FEATURES
   DEFINITION
  Matches
   Query Match
Best Local Similarity
  source
  249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
   189
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
   N
  Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
Email: estewartson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 904 Std Error: 0.00
Seq primer: mob.REGA+ET
  The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School c 4444 Forest Park Parkway, Box
  Hominidae; Homo.

1 (bases I 676)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Kucaba.T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Williamson,A., Wohldmann,P. and
Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P.
  W56120.1 GI:1358009
EST.
   W56120 576 bp mRNA linear EST 11-OCT-1990 zc56h06.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   Bukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homo sapiens
  Homo sapiens (human)
  (HUMAN);, mRNA sequence.
  CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG
   cuentrucceaaanccaecuearecaceueeueeueeueeueeucueaacuccaueeaaceue
  quality sequence stop: 433.
Location/Qualifiers
  Conservative
TTTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5 Library constructed by Bento soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
   /organism="Homo sapiens"
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  /clone="IMAGE:326363"
  51.4%;
   ; Score 47.8; DB 8; ; Pred. No. 5e-05; 15; Mismatches 27;
   of Medicine
x 8501, St. Louis,
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  Indels
  ð
  63108
   EST 11-OCT-1996
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   61
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RESULT W56120 LOCUS

밁 Ş В Ś ORIGIN

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10:36:37 2005
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TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
```

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```
ACCESSION
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W39202
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   SOURCE
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Best Local :
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   ORGANISM
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  184 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
  W39202 583 bp mRNA linear EST 15-MAY-1990
zb35h03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:305621 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
  2 cuguruccganauccagcugaugcacgguggugguggugguggugaacguccauggaacgug 61
   49;
   Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET
   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkina,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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  Similarity
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   The WashU-Merck EST Project
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Matches

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Conservative

15;

Indels

0

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1 (Dases 1 to 721)

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Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,

Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,

Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
   Homo sapiens
   Email: scain@athersys.com
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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  Tel: 216 431 9900
Fax: 216 361 9596
   Athersys, Inc.
  Contact: Scott J. Cain
   Similarity
  3201 Carnegie Ave, Cleveland,
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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www-bio.llnl.gov/bbrp/image/lmage.html
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High quality sequence stop: 444.
Location/Qualifiers
  Contact: Robert Strausberg, Ph.D.
Email: ggapbs-remail.nih.gov
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L Unpublished (2003)

L Contact: Ina Rolls

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

IM Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAG9998J24728

RZPDLIB; I.M.A.G.E. CDNA Clone Collection;

Human Unigeneset - RZPDLIB NO.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showlib_pl.cgi/response?iibNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111
  210 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 269
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   Dases 1 to 757)

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Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.

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BX106232
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Location/Qualifiers
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Search completed: November 24, 2005, 01:30:28 Job time : 1825 secs

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US-08-468-275-3 RESULT 2

Sequence 3, Application US/08468275
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APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING
TITLE OF INVENTION: ELECTROTRANSPORT FLUX
NUMBER OF SEQUENCES: 10

OF POLYPEPTIDES

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62

62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU TTGAATGGCTGCGTAAAAAACTGCAGGATGTT

| D O US. S G G G G G G G G G G G G G G G G G G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | oο                                                                                                                                |
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| Sequence 11793, A Sequence 21712, A Sequence 22, Appl Sequence 31, Appl Sequence 31, Appl Sequence 24, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 20, Appl Sequence 30, | 5, Appli<br>6, Appli<br>6, Appli<br>18519, A<br>18519, A<br>51, Appl                                                              |

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  US-08-468-275-3
  NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: MUCLEIC acid
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   Sequence 5, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-UNN-1995
CLASSIFICATION: 514
CCLASSIFICATION: 514
   TOPOLOGY: lir
MOLECULE TYPE:
FEATURE:
   FEATURE: mat_peptide LOCATION: 25
  ATTORNEY/AGENT INFORMATION: NAME: MILLER, D. BYRON
  STREET: 950 PAGE MILL ROAD CITY: PALO ALTO STATE: CALIFORNIA
  COUNTRY:
  LOCATION:
   NAME/KEY:
   COUNTRY: USA
ZIP: 94303-0802
  86 TIGAATGGCTGCGTAAAAAACTGCAGGACGT 116
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   26 CCGTTTCCGAAATCCAGCTGCTCCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85
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56; Conservative
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGAACCUCCAUGGAACGUG 61
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7..138
  DNA (genomic)
   68.6%; Score 63.8; DB 2; 61.5%; Pred. No. 1.7e-12; tive 18; Mismatches 17;
   O360-0002; ARC-2349
   Length 141;
  Indels
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В
  RESULT 4
US-09-007-466-3
  US-08-468-275-5
  REFERENCE/DOCKET NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
   Sequence 3
Patent No.
  Matches
   Query Match
Best Local
  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: USA
  GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
TELEPHONE: (415) 496-80150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-UUN-1995
ATTORNEY/AGENT INFORMATION:
  ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,466
  NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 033
REFERENCE/FOCKET NUMBER: 033
REFERENCE/FOCKET NUMBER: 031
REFERENCE/FOCKET NUMBER: 030
REFERENCE/FOCKET NUMBER
  MOLECULE TYPE: DNA (genomic)
  ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
   STRANDEDNESS: si:
TOPOLOGY: linear
  FILING DATE: 0 CLASSIFICATION:
  116 CCGTTTCCGAAATCCAGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57
  56 TTGAATGGCTGCGTAAAAACTGCAGGACGT 26
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
  56; Conservative
  2 cuguuuccgaaauccagcugaugcacgguggugguggugguggaacuccauggaacgug 61
   H: 141 base pairs nucleic acid DEDNESS: single
   , Application US/09007466 6313092
  h 68.6%; Score 63.8; DB 2;
Similarity 61.5%; Pred. No. 1.7e-12;
56; Conservative 18; Mismatches 17;
   06-JUN-1995
   US 08/468,275
  US/08/468,275
  O360-0002; ARC-2349
   O360-0002; ARC-2349
  Gaps
  0
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nucleic acid

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   RESULT 5
US-09-007-466-5/c
  밁
  US-09-007-466-3
   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
   Sequence 5, Application US/09007466 Patent No. 6313092
  Matches
   Best Local
  Query Match
Best Local Similarity
Matches 56; Conserv
                              Query Match
  GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
  FEATURE:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/007,466
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  NAME/KEY:
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  STREET: 950 PAGE CITY: PALO ALTO
   STRANDEDNESS:
TOPOLOGY: 111
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   26
   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
   94303-0802
   Similarity
  CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85
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  950 PAGE MILL ROAD
  USA
  Conservative
   CDS
7..138
  mat_peptide
25
68.6%; Score 63.8; DB 3; llarity 61.5%; Pred. No. 1.7e-12; Conservative 18; Mismatches 17
   linear
   ALZA CORPORATION
   DNA (genomic)
  single
   METHOD FOR INCREASING THE ELECTROTRANSPORT FLUX OF POLYPEPTIDES
   68.6%; Score 63.8; DB 3; 61.5%; Pred. No. 1.7e-12;
   10
  US 08/468,275
  18; Mismatches
  O360-0002; ARC-2349
                                DB 3; Length 141;
   17;
  Length 141;
   Indels
   Indels
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   0,
   Gaps
   0
   0
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  δ
   US-08-952-980B-3
  RESULT 6
   US-08-952-980B-3
  Sequence 3, Application US/08952980B Patent No. 6333189
   Matches
  Query Match
  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
NAME: MILLER, D. BYRON
   TELEFAX: (650) 496-804
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  GENERAL INFORMATION:
APPLICANT: HOLLAD
  FEATURE:
NAME/KEY:
LOCATION:
   STREET: 930 ALTO CITY: PALO ALTO CALIFORNIA TICA
  APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF E
   REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 496-8150
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
   FEATURE:
  MOLECULE TYPE:
  NUMBER OF SEQUENCES:
  TELEPHONE: (650) 4
   ZIP: 94303-0802
  Match 68.6%; Score 63.8; DB 3; Local Similarity 61.5%; Pred. No. 1.7e-12; es 56; Conservative 18; Mismatches 17;
   LOCATION:
  NAME/KEY:
   TOPOLOGY:
  STRANDEDNESS:
  LENGTH:
   116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGGGTG
   56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
98
  2 cugurucceanauccaecueauecaecueeueeueeueeueueueaaeueeaaaeeue
   nucleic acid
  cugurucceaaanuccaecugaugeacecugeugeugeuceucaaacuccaugeaaceue
 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
   950 PAGE MILL ROAD
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7..138
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25
   linear
  umBER: US/08/952,980B
20-NOV-1997
  DNA (genomic)
  single
  496-8048
   ELECTROTRANSPORT FLUX OF POLYPEPTIDES
   ω
..
  2349 CIP 1
  Version #1.30
   92
   Length 141;
   Indels
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   Gaps
  57
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  85
  61
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RESULT 7 US-08-952-980B-5/c

; Sequence 5, Application US/08952980B

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   Ś
  В
  Ś
   US-08-142-551B-8
   TELEFAX: (650) 496-8048
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
   Sequence 8, Application US/08142551B Patent No. 5814603 GENERAL INFORMATION:
  Patent No. 6333189
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING
TITLE OF INVENTION: ELECTROTRANSPORT FLUX
NUMBER OF SEQUENCES: 12
   Query Match
Best Local
   Matches
   ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 2349
TELECOMMUNICATION INFORMATION:
TELECHIONE: (650) 496.8150
  ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIFICATION: 530
CLASSIFICATION: 530
   APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   CORRESPONDENCE ADDRESS
  STREET: 950 PAGE MILL ROAD CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
  STREET: 699 Prince Street CITY: Alexandria STATE: Virginia
   COUNTRY:
   ADDRESSEE:
  ADDRESSEE:
   Local
   116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
::|||:|||:|||:|||||||:|||||:||
56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26
   ch 68.6%;
1 Similarity 61.5%;
56; Conservative 1
   2 cugurucceaaauccaecueauccaecuecuecuecuecuecueaacuccauceaaccue 61
   22313
   Burns,
  ALZA CORPORATION
   Doane, Swecker & Mathis
   Score 63.8; DB 3; Pred. No. 1.7e-12; 18; Mismatches 17;
  2349 CIP 1
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   Gaps
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US-08-733-446-58
Sequence 58, Application US/08733446
Patent NO. 5865138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS
TITLE OF INVENTION: PRODUCTION THEREOF
NUMBER OF SEQUENCES: 62
  Ś
   Ď,
  Ś
  В
   US-08-142-551B-8
   RESULT 9
   APPLICATION NUMBER: US 07/965
APPLICATION NUMBER: US 07/965
PILING DATE: 22-0CT-1992
AFTORNEY/AGRNT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 0003
REFERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (4.15) 854-7400
TELEPHAX: (4.15) 854-8275
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
   Matches
  Query Match
Best Local
  PEATURE:
NAME/KEY: misc_feature
LOCATION: 70..174
OTHER INFORMATION: /note
OTHER INFORMATION: pepti
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LOCATION: 1..51
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  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-UW-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
  NAME/KEY: misc_feature LOCATION: 175..207
OTHER INFORMATION: /note OTHER INFORMATION: havii
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ORRESPONDENCE ADDRESS
   FILING DATE: 2:
CLASSIFICATION:
  131
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   1 Similarity 61.5 56; Conservative
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGUCGAACCUCCAUGGAACGUG 61
   1..201
  CDS
  25-OCT-1993
   68.6%; Score 63.8; D
61.5%; Pred. No. 1.9e
tive 18; Mismatches
  /note= "Encodes amino acid sequence
having six histamines that serves as a tag for the
purification of the protein on a nickel column."
  /note= "Encodes the leader peptide
sequence that serves to direct the
inclusion bodies."
   /note= "Encodes the protein
peptide of interest"
  US 07/965,677
   000324-010
  DB 2;
..9e-12;
   .25
   Length 207
   Indels
  õ
   AND
   protein into
   0
   Gaps
   0,
```

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RESULT 10
US-10-340-484-14
   밁
  ঠ
   밁
  S
   US-08-733-446-58
  GENERAL INFORMATION: Andrew F.
APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
CURRENT EPLICATION NUMBER: US/10/340,484
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR APPLICATION NUMBER: 60/353,296
PRIOR APPLICATION NUMBER: 60/353,296
   Sequence 14, Application US/10340484 Patent No. 6875739
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  APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
  TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPAX: (617) 523-6440
  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  ATTORNEY/AGENT INFORMATION:
  OLECULE TYPE:
  LOCATION:
NAME/KEY:
LOCATION:
  ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN STREET: 130 Water Street CITY: Boston
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   LENGTH: 252 base pairs
TYPE: nucleic acid
   NAME: NEUNER, George
REGISTRATION NUMBER:
   COUNTRY:
  STATE: Massachusetts
   LOCATION: 19...24
IDENTIFICATION METHOD:
   NAME/KEY:
  TOPOLOGY:
   STRANDEDNESS:
APPLICATION NUMBER: 60/368,955
   62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   N
  2 сисилиссерадиссассисаниста советсение в поставительного пост
   50; Conservative
   02109
   Similarity
   CTGTGTCCGAGATTCAGCTGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG
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  other nucleic acid, synthetic DNA
   double
  2002-02-01
   58.3%; Score 54.2; DB 2; Length 252; 54.9%; Pred. No. 4e-09; ative 18; Mismatches 23; Indels
   26964
   (F)
   42025
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   Gaps
   61
  61
   0
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-340-484-14
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   US-08-689-190-1
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  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSITETION OF THE PROPERTY OF THE PROPER
   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 14
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  Matches
  Best
  Query Match
  TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
   GENERAL
   PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 27
   LENGTH:
   REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
   APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: U
   TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN TITLE OF INVENTION: PARATHYROID HORMONE NUMBER OF SEQUENCES: 18
  CORRESPONDENCE ADDRESS:
  APPLICANT:
  APPLICANT:
   FILING DATE:
APPLICATION NUMBER:
FILING DATE:
   ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN STREET: 130 Water Street
   TELEPHONE: (617)523-6440
  Local Similarity
   COUNTRY:
   STRANDEDNESS:
   TOPOLOGY:
  INFORMATION:
   62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   102
  49;
   Boston
   cuguruccgaaauccagcugaugcacggugguggugguggugucugaacuccauggaacgug 61
   CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61
   Massachusetts
  YAMADA, Takao
  OSHIKA, Yuri
  Conservative
other nucleic acid, synthesizing DNA
   double
  Tsunehiko
  56.6%; Score 52.6; DB 3; 53.8%; Pred. No. 1.1e-08;
  US/08/016,171
  US/08/006,197
  18;
   41,288
  Mismatches
  Length 102;
  Indels
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  Gaps
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US-08-733-446-23
US-08-733-446-23
Sequence 23, Application US/08733446
Sequence 13, Explication US/08733446
Patent NO. 5856138
GENERAL INFORMATION:
FOUNDAL TSUMBHING
TITLE OF INVENTION: HUWAN PARATHYRE
TITLE OF INVENTION: PRODUCTION THEI
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
  밁
   Ś
   밁
  8
  ; FEATURE:

, NAME/KEY: MUTATION

; LOCATION: 7, 8, 9, 12, 15, 19,

; IDENTIFICATION METHOD: S

US-08-689-190-1
   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
   Query Match 56.6%;
Best Local Similarity 53.8%;
Matches 49; Conservative 1
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/402,970
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
  ATTING DATE:
ATTOMEY AGENT INFORMATION:
ANAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 4202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
   MOLECULE TYPE:
  NAME/KEY: CDS
LOCATION: 1..252
IDENTIFICATION METHOD:
  TELEFAX:
   STREET:
IDENTIFICATION METHOD:
  COUNTRY:
   ADDRESSEE:
   ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
  2 cugurucceaaauccaecueauecaceueeueeueeueeucueaacuccaueeaaceue 61
  Boston
   02109
  Massachusetts
   130 Water Street
  (617)523-6440
   other nucleic
  , Tsunehiko
: HUMAN PARATHYROID HORMONE MUTEINS AND
: PRODUCTION THEREOF
   23:
  (H)
   18;
   42025
   Score 52.6; DB 2;
Pred. No. 1.4e-08;
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   33, 36, 43, 51, 58,
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   밁
   US-08-733-446-23
  US-08-733-446-56
  RESULT 13
   US-08-733-446-56
   NAME: NEUNER, George W
REGISTRATION NUMBER: 2694
REFERENCE/DOCKET NUMBER: 4202!
TELECOMMUNICATION INFORMATION:
TELECHOUS: (617)523-400
TELEFAX: (617)523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: other nucleic ac:
   Query Match
Best Local Similarity 53.8
Matches 49; Conservative
   Sequence 56, Applicat Patent No. 5856138 GENERAL INFORMATION: APPLICANT: FUKUDA
Query Match 56.6%; Score 52.6; DB 2; Length 252; Best Local Similarity 53.8%; Pred. No. 1.4e-08; Matches 49; Conservative 18; Mismatches 24; Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/733,446
FILLING DATE: 18-OCT-1996
  APPLICATION NUMBER: US/07/926,787 FILING DATE: ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
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  TITLE OF INVENTION:
   NUMBER OF SEQUENCES:
   LOCATION:
NAME/KEY:
LOCATION:
  NAME/KEY: mutation LOCATION: 103...105 IDENTIFICATION METHOD:
   CITY: Boston
   NAME/KEY:
   ADDRESSEE: DAVID G
ADDRESSEE: CUSHMAN
   62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
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  5, Application US/08733446
5856138
  Massachusetts
  130 Water Street
   CDS
  1..252
  other nucleic acid, synthetic DNA
  A, Tsunehiko

HUMAN PARATHYROID HORMONE MUTEINS AND

HERODUCTION THEREOF
  G. CONLIN; DIKE, BRONSTEIN, ROBERTS
  56.6%; Score 52.6; DB 2; 53.8%; Pred. No. 1.4e-08; tive 18; Mismatches 24;
   US/08/402,970
  42025
  24;
  Length 252;
  Indels
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  Gaps
   61
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Gaps

```
RESULT 14
US-08-835-231-34
  á
  밁
   ; NAME/KEY:
; LOCATION:
US-08-835-231-34
  TELEX: 61/----
TELEX: 200291 STRE
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
YENGTH: 252 base pairs
   Sequence 34,
Patent No. 5
Query Match
Best Local Similarity
  FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
APPLICATION NUMBER: JP 0271438
APPLICATION NUMBER: JP 0271438
  GENERAL INFORMATION:
  ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 4161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
   MOLECULE TYPE: Synthetic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
   APPLICANT: KURIYAMA, Masato
APPLICANT: KOYAMA, No. 5861284uyuki
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
NUMBER OF SEQUENCES: 37
  FEATURE:
  SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
   APPLICANT:
   TYPE: nucleic acid
STRANDEDNESS: double
  APPLICATION NUMBER:
   COUNTRY:
  ORGANISM:
  TOPOLOGY:
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
  N
  02109
  BOSTON
   TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
  CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG
   cugurucceananuccaecueanecaceueeueeueeueeucueaacuccaueeaaceue 61
  ₹
   Application US/08835231
   USA
   NISHIMURA, Osamu
KURIYAMA, Masato
  linear
  IBM Compatible
SYSTEM: DOS
  Synthetic DNA
  Coding Sequence
1...252
56.6%;
  US/08/835,231
  34:
   41614-FWC
  Score 52.6; DB 2;
Pred. No. 1.4e-08;
                  Length 252;
  61
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   멍
  밁
   US-09-108-661-34
US-09-108-661-34
   Sequence 34, App. No. 628780
   GENERAL INFORMATION:
APPLICANT: NISHIMU
APPLICANT: KURIYAM
APPLICANT: KOYAMA,
  Matches
  TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 3
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APPLICATION NUMBER: 07/838,857
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S.
NAME: DAVID, RESNICK S.
             FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Synt
FEATURE:
NAME/KEY: Codi
LOCATION: 1...
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM COMPATE
COMPUTER: COMPATEM: DO
COMPUTER: COMPATEM: DO
   APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
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   MOLECULE TYPE: S
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   STREET: 130 1
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   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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  49; Conservative
   CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG
  ¥
  Application US/09108661
  130 WATER STREET
   USA
  NISHIMURA, Osamu
KURIYAMA, Masato
  KOYAMA,
  ŏ
   linear
  Synthetic DNA
  IBM Compatible
                 Coding Sequence
1...252
   DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   Diskette
  Synthetic DNA
   double
  No. 6287806uyuki
   us/09/108,661
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  18; Mismatches
  24;
   Indels
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  Gaps
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Maximum DB seq length: 200000000
  Total number of hits satisfying chosen parameters:
  Searched:
   Scoring table:
  Sequence:
   Perfect score:
  Title:
   Run on:
  OM nucleic - nucleic search, using sw model
  Post-processing:
Published Applications NA Main:*

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2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*
           November 23, 2005, 23:59:22; Search time 412.667 Seconds (without alignments) 1863.616 Million cell updates/sec
   1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93
   US-09-475-158A-14
93
  9793542 segs, 4134689005 residues
  Gapop 10.0 , Gapext 1.0
  IDENTITY_NUC
  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
  19587084
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| 23                | 22                | 21                | 20                | 19                | 18                | 17                | 16               | 15               | 14               | 13               | 12                | 11                | 10                | 9                 | 8                 | 7                 | 6                | <sub>U</sub>      | 4.               | w                 | 2                 | ۲                | Result<br>No. |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|------------------|---------------|
| 53.8              | 57.4              | 57.4              | 68                | 68                | 68                | 69.6              | 69.6             | 69.6             | 69.6             | 69.6             | 69.6              | 69.6              | 69.6              | 69.6              | 69.6              | 69.6              | 69.6             | 69.6              | 69.6             | 69.6              | 69.6              | 69.6             | Score         |
| 57.8              | 61.7              | 61.7              | 73.1              | 73.1              | •                 |                   | •                | 74.8             |                  | 74.8             |                   | 74.8              |                   | 74.8              | 74.8              | 74.8              | 74.8             | 74.8              | 74.8             | 74.8              | 74.8              | 74.8             | Query         |
| 106               | 945               | 717               | 489               | 489               | 489               | 426               | 420              | 321              | 291              | 291              | 282               | 276               | 276               | 276               | 264               | 252               | 252              | 117               | 111              | 111               | 102               | 102              | Length        |
| w                 | Ф                 | Ф                 | თ                 | σ                 | σ                 | ø                 | 9                | ø                | ø                | 9                | 9                 | 9                 | 9                 | 9                 | 9                 | 9                 | 9                | 9                 | 9                | 9                 | 9                 | 9                | В             |
| US-09-746-945-11  | US-10-848-279-8   | US-10-848-279-7   | US-10-407-078-43  | US-10-407-078-14  | US-10-117-109-14  | US-10-997-762-20  | US-10-997-700-93 | US-10-997-700-91 | US-10-997-700-77 | US-10-997-700-76 | US-10-997-078-133 | US-10-997-700-75  | US-10-997-822-3   | US-10-997-762-18  | US-10-997-700-89  | US-10-997-700-35  | US-10-997-078-62 | US-10-997-078-141 | US-10-997-700-34 | US-10-997-078-61  | US-10-997-700-33  | US-10-997-078-60 | ID            |
| Sequence 11, Appl | Sequence 8, Appli | Sequence 7, Appli | Sequence 43, Appl | Sequence 14, Appl | Sequence 14, Appl | Sequence 20, Appl | •                | •                | -                |                  | Sequence 133, App | Sequence 75, Appl | Sequence 3, Appli | Sequence 18, Appl | Sequence 89, Appl | Sequence 35, Appl | _                | _                 |                  | Sequence 61, Appl | Sequence 33, Appl | -                | Description   |

GENERAL INFORMATION:

|                                          |                    |                  |                  |                  |                  |                  |                  |                  |                  |                  |                   |                  |                  |                 |                 |                 |                 |                 |                 | a                |
|------------------------------------------|--------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|
| 4 4<br>5 4                               | 43                 | 42               | 41               | 40               | 39               | 38               | 37               | 36               | 36               | 34               | 33                | 32               | 31               | 30              | 29              | 28              | 27              | 26              | 25              | 24               |
| 47.8<br>47.8                             | 47.8               | 47.8             | 47.8             | 47.8             | 47.8             | 47.8             | 47.8             | 47.8             | 47.8             | 47.8             | 47.8              | 51               | 52.6             | 53.6            | 53.6            | 53.6            | 53.6            | 53.6            | 53.6            | 53.8             |
| 51.4                                     | 51.4               | 51.4             | 51.4             | 51.4             | 51.4             | 51.4             | 51.4             | 51.4             | 51.4             | 51.4             | 51.4              | 54.8             |                  | 57.6            | 57.6            | 57.6            | 57.6            | 57.6            | 57.6            | 57.8             |
| 102                                      | 102                | 102              | 102              | 102              | 102              | 102              | 102              | 102              | 102              | 102              | 102               | 258              | 102              | 874             | 874             | 432             | 432             | 348             | 348             | 107              |
| စ ဖ                                      | 9                  | 9                | 9                | ø                | 9                | 9                | 9                | 9                | 9                | 9                | 9                 | œ                | σ                | 6               | σ               | σ               | σ               | σ               | 6               | w                |
| US-10-775-204-1435<br>US-10-775-204-1386 | US-10-775-204-1434 | US-10-775-204-72 | US-10-775-204-69 | US-10-775-204-64 | US-10-775-204-61 | US-10-775-204-60 | US-10-775-204-57 | US-10-775-204-52 | US-10-775-204-51 | US-10-775-204-25 | US-10-775-204-24  | US-10-343-189-15 | US-10-340-484-14 | US-10-359-091-7 | US-10-437-038-7 | US-10-359-091-3 | US-10-437-038-3 | US-10-359-091-1 | US-10-437-038-1 | US-09-746-945-12 |
| Sequence 1435<br>Sequence 1386           | Sequence 1434      | Sequence 72,     | Sequence 69,     | Sequence 64, 1   | Sequence 61, F   | Sequence 60, A   | Sequence 57, A   | Sequence 52, A   | Sequence 51, A   | Sequence 25, A   | Sequence 24, Appl | Sequence 15, A   | Sequence 14, A   | Sequence 7, Ap  | Sequence /, Ap  | ٠,              |                 | , <u>-</u>      | ۲,              | . 1.             |

## ALIGNMENTS

RESULT 1

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US-10-99-078-60

; Sequence 60, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
RESULT 2
US-10-997-700-33
; Sequence 33, Application US/10997700
; Publication No. US20050239172A1
   Ş
  밁
  Ś
  ; FEATURE:
; OTHER INFORMATION: PTH(1-34).
US-10-997-078-60
   APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
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SEQ ID NO 60
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Matches 58; Conserv
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TYPE: DNA
ORGANISM: Unknown
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUCGAACCUCCAUGGAACGUG 61
   TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
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   74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 2.6e-15; rative 20; Mismatches 14;
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  Gaps
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RESULT 3
US-10-997-078-61
US-10-997-078-61
Sequence 61, Application US/10997078
Publication No. US20050221444A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Yean, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.010US1
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US/10/997,078
CURRENT APPLICATION NUMBER: US/643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 111
TYPE: NAM
  유 성
   밁
   ; FEATURE:
; OTHER INFORMATION: PTH(1-37).
US-10-997-078-61
  Ś
  ; FEATURE:
; OTHER INFORMATION: PTH(1-34).
US-10-997-700-33
  Ś
   밁
   ş
  Query Match
Best Local S
Matches 58
   APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REPERBURGE: 1627-009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
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   Query Match
Best Local (
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  62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:||||||||||::
62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
   N
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  Similarity
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  74.8%; Score 69.6; DB 9; ilarity 63.0%; Pred. No. 2.6e-15; Conservative 20; Mismatches 14;
  74.8%; Score 69.6; DB 9; larity 63.0%; Pred. No. 2.7e-15; Conservative 20; Mismatches 14;
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Sequence 141, Applicat;
Publication No. US2005(
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Xia, U.
   APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
FILE REFERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-997-078-141
  á
  멍
   ; OTHER INFORMATION: PTH(1-37). US-10-997-700-34
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; GENERAL INFORMATION:
APPLICANT: Wagner, F
APPLICANT: Peng, L
; APPLICANT: Holmquis
   US-10-997-700-34
  US-10-997-078-141
  APPLICANT: Holdquist, B.
APPLICANT: Holdquist, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
FILE REPERENCE: 1627 0,10161
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
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PRIOR PRILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
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Indels

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APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Peng, L.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION Methods and DNA Constructs for FILE REFERENCE: 1627-0.10US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PTUING JATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION PRIOR STATES CONTROL SERVING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
   á
   밁
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  밁
  RESULT 6
US-10-997-078-62
S
   APPLICANT: Xia U.

APPLICANT: Holmquist, B.

APPLICANT: Holmquist, B.

TITLE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627,009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
   US-10-997-700-35
  RESULT 7
  밁
   á
  ; OTHER INFORMATION: PTH(1-84) US-10-997-078-62
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LENGTH: 252
TYPE: DNA
ORGANISM: Unknown
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  Sequence 62, Applica Publication No. US20 GENERAL INFORMATION:
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   Sequence 35, Application US/10997700 Publication No. US20050239172A1
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  Query Match
Best Local Similarity
  APPLICANT: Wagner, F. APPLICANT: Peng, L. APPLICANT: Xia, U.
OTHER INFORMATION:
  TYPE: DNA
ORGANISM: Unknown
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   N
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  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   uugaauggcugcguaaaaaacugcaggacguu 93
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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  Length 252;
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   Production of Polypept
  61
   of Polypept
   0;
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  5
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   8
   밁
   US-10-997-762-18
  RESULT 9
   OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84)
US-10-997-700-89
  US-10-997-700-89
  RESULT
   APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
TITLE REFERENCE: 1627.009US1
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER: OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 264
  Sequence 89, Application US/10997700
publication No. US20050239172A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
  Matches
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   Sequence 18, Application US/10997762 Publication No. US20050227313A1
   Matches
  Query Match 74.8%;
Best Local Similarity 63.0%;
   APPLICANT: Seo, Jin Seog
APPLICANT: Strydom, Daniel
APPLICANT: Holmquist, Barton
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REFERENCE: 1627.026US1
   CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
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   2 cugurucceaaauccaecueauecaceueeueeueeueeucueaacuccaueeaaceue
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  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64
   TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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  74.8%;
  74.8%;
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   20; Mismatches
  Score 69.6; DE Pred. No. 3.3e-20; Mismatches
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Pred. No. 3.4e-15;
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GENERAL INFORMATION:

APPLICANT: Holmquist, B.

APPLICANT: Holmquist, B.

APPLICANT: Gensalk, X.

APPLICANT: Cryer, P.

INVENTON: POLYPEPTIDE CLEAVAGE PROCESS

FILE REFERENCE: 1627.011US: 105/10/997,822

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: PCT/US03/16647

PRIOR APPLICATION NUMBER: US 60/383,484

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 3

LENGTH: 276
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US-10-997-700-75
  밁
   á
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  밁
   δ
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   Ś
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  ; OTHER INFORMATION: Nucleotide sequence of a US-10-997-822-3
Sequence 75, Application US/10997700
Publication No. US20050239172A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Yeng, L.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627,009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION SUMMER: US 60/383,212
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Best Local Similarity 63.1
Matches 58; Conservative
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   Query Match
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ORGANISM: Artificial Sequence
   FEATURE:
  ORGANISM: Artificial Sequence
  FEATURE:
  Local Similarity
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  233
   233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:|||||:||
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
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  74.8%;
   74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 3.4e~15; tive 20; Mismatches 14;
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Pred. No. 3.
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  DB 9;
.4e-15;
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   Length
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  RESULT 12
US-10-997-078-133
   밁
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  RESULT 13
US-10-997-700-76
  Ş
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   Ş
   ; FEATURE:
; OTHER INFORMATION:
US-10-997-078-133
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   Ś
  밁
   Query Match
Best Local S
Matches 58
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Matches 58
                     Sequence 76, Application US/10997700
Publication No. US20050239172A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
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  227 TTGAATGCCTGCGTAAAAAACTGCAGGACGTT 258
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  74
   62
   14
   58;
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  Similarity
  Similarity
  Peng, I
      Holmquist,
  Þ
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APPLICANT: Restoragen, Inc.
ITITLE OF INVENTION: Methods and DNA Constructs for ITITLE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627-010US1
CURRENT FILING DATE: 2004-11-24
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-05-24
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 133
LENGTH: 282
TYPE: DNA
ORGANISM: Artificial Sequence
  Sequence 133, Application US/10997078
Publication No. US20050221444A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
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SEQ ID NO 75
LENGTH: 276
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UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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   Conservative
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   74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 3.4e-15; tive 20; Mismatches 14
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  sequence for the T7tagVg-PTH(1-34)
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   14;
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   for High Yield Production of Polypeptic
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   Gaps
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  61
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APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
ITITE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 291
  RESULT 15
US-10-997-700-91
  ş
  RESULT 14
US-10-997-700-77
   밁
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  용
   ঠ
   밁
  밁
   δ
   ) OTHER INFORMATION: A US-10-997-700-76
  Sequence 77, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 291
TYPE: DNA
Sequence 91, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
   Query Match
Best Local Similarity
   Matches
   Query Match
Best Local Similarity
   Matches
  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.009US1 CURRENT APPLICATION NUMBER: US/10/997,700 CURRENT FILING DATE: 2004-11-24 PRIOR APPLICATION NUMBER: US 60/383,212 PRIOR FILING DATE: 2002-05-24 NUMBER OF SEQ ID NOS: 93
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   89
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   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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Xia, U.
   Conservative
   Sequence
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  Score 69.6; DB 9;
Pred. No. 3.4e-15;
20; Mismatches 14;
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  Gaps
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  88
   of Polypept
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APPLICANT: Wagner, F.

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; FEATURE:
; OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH(1-84).
US-10-997-700-91
   APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
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TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 153
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   74.8%;
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0; Mismatches 14;
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Result
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Maximum DB
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   Total number of hits satisfying chosen parameters:
  Searched:
   Scoring table:
  sequence:
  Perfect score:
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9
110
111
112
113
113
114
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119
120
221
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
26.8
25.2
  seq length: 0 seq length: 2000000000
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   Published_Applications_NA_New:*

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   Maximum Match 100%
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320
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US-10-821-231-760
US-10-1184-005-23
US-10-118-826A-351
US-10-119-826-351
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Sequence 351, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 315, Appl
Sequence 315, Appl
Sequence 315, Appl
Sequence 4301, Appl
Sequence 112, Appl
Sequence 112, Appl
Sequence 125, Appl
Sequence 19, Appl
Sequence 31, Appl
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  Sequence
  2, Appli
760, App
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  US-11-167-273-2
  Sequence 2, Application US/11167273
publication No. US2005025567A1
GENERAL INFORMATION:
APPLICANT: GUSYATINER, Mikhail Markovich
APPLICANT: IVANOVSKAYA, Lirina Valerievna
APPLICANT: LEONOVA, Tatyana Viktorovna
APPLICANT: MUKHANOVA, Ekaterina Igorevna
APPLICANT: ROSTOVA, Yulia Georgievna
APPLICANT: ROSTOVA, Yulia Georgievna
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|-------------------------------------------------------------|---------------------------------------------------------------------------------------------------|------------------------------------------------------------|-----------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|
| 7.50                                                        | 440                                                                                               | 760                                                        | 3 2 2 3                                                   | 30<br>31                                                                         | 4000                                                                             |
| 222                                                         | 20.2<br>20.2<br>20.2                                                                              | 20.2                                                       | 20.4                                                      | 0000<br>0000                                                                     | 21.2<br>21.2<br>21.2                                                             |
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| 1542<br>1929<br>3719                                        | 1606<br>1606<br>5412<br>40439<br>809                                                              | 1208                                                       | 1189<br>5506                                              | 7893<br>8106<br>23907<br>24120                                                   | 636<br>636<br>1910<br>11337                                                      |
|                                                             | 8111                                                                                              | , r r <                                                    | 1 12 12 V                                                 | 7777                                                                             | ם ש ש ש                                                                          |
| US-10-990-276-4<br>US-10-821-234-50<br>US-10-131-826A-49    | US-10-131-8264-85<br>US-10-131-8264-257<br>US-10-821-234-36<br>US-10-993-509-1<br>US-11-132-839-6 | US-10-821-234-290<br>US-10-821-234-290<br>US-10-858-730-53 | US-11-033-764-19<br>US-10-821-234-83<br>US-10-821-234-277 | US-11-186-731-3<br>US-11-186-731-1<br>US-11-186-731-6<br>US-11-186-731-4         | US-10-842-206-1<br>US-10-980-459-8<br>US-10-821-234-211<br>US-10-499-715-1       |
| Sequence 4, Appli<br>Sequence 50, Appl<br>Sequence 49, Appl | Sequence 257, App. Sequence 36, App. Sequence 1, App.1. Sequence 6, App.1.                        |                                                            |                                                           | Sequence 3, Appli<br>Sequence 1, Appli<br>Sequence 6, Appli<br>Sequence 4, Appli | Sequence 1, Appli<br>Sequence 8, Appli<br>Sequence 211, App<br>Sequence 1, Appli |

## ALIGNMENTS

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FILE REFERENCE: 230720US0

CURRENT APPLICATION NUMBER: US/11/167,273

CURRENT FILING DATE: 2005-06-28

PRIOR APPLICATION NUMBER: US/10/299,799

PRIOR FILING DATE: 2002-11-20

PRIOR APPLICATION NUMBER: RU 2001132473

PRIOR FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 1410

TYPE: DNA

ORGANISM: Escherichia coli

US-11-167-273-2
   RESULT 2
US-10-821-234-760/c
GENERAL INFORMATION:
                  Sequence 760, Application US/10821234
Publication No. US20050255114A1
   Matches
  Query Match
Best Local Similarity
   APPLICANT: FILIPPOV, Dmitriy Vladmirovich
APPLICANT: CHUDAKOVA, Daria Aleksandrovna
TITLE OF INVENTION: NEW MUTANT GLUTAMINE SYNTHETASE AND METHOD FR PRODUCING AMINO ACII
  1182 CÁAAAACCTGTATGACCT 1199
   15 CCAGCUGAUGCACGGUGGUGGUGGUCGUCGAACUCCAUGGAACGUGUUGAAUGGCUGCG 74
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US-11-184-005-23/c

| Sequence 23, Application US/11184005
| Publication No. US20050256052A1
| GENERAL INFORMATION:
| APPLICANT: Luyten, Frank P.
| APPLICANT: Moos, Malcolm JR.
| APPLICANT: Hoang, Bang
| APPLICANT: Hoang, Bang
| APPLICANT: Wang, Shouwen
| TITLE OF INVENTION: METHOD OF MODULATING TISSUE
| TITLE OF INVENTION: GROWTH USING FRZE PROTEIN
| FILE REFERENCE: NITAL33.1CPC3
| CURRENT APPLICATION NUMBER: US/11/184,005
  Sequence 4, Application US/10526731

| Publication No. US20050244437A1
| GENERAL INFORMATION:
| APPLICANT: AKZO NObel N.V. |
| TITLE OF INVENTION: live attenuated parasite vac |
| FILE REFERENCE: 2002-017-EP |
| CURRENT APPLICATION NUMBER: US/10/526,731 |
| CURRENT APPLICATION NUMBER: BP 02078953 |
| PRIOR APPLICATION NUMBER: EP 02078953 |
| PRIOR FILING DATE: 2002-09-20 |
| NUMBER OF SEQ ID NOS: 29 |
| SOFTWARE: PatentIn version 3.2 |
| SEQ ID NO 4 |
| LENGTH: 2748 |
| TYPE: DNA |
| ORGANISM: Toxoplasma gondii |
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  RESULT 3
US-10-526-731-4
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   В
   Ş
  Ś
  FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DC_SEQ_Genes Version 1.0
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ORGANISM: Homo sapiens
-10-821-234-760
   APPLICANT: Labat, Ivan
APPLICANT: Stache-Cra:
APPLICANT: Andarmani,
APPLICANT: Tang, Y. To
   APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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   2021 GTGGTCTGTGCGCCÁTGGCÁCAGGCAGAÁTCGTTGCGGTACAAGCTTC 2068
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  834 GAGGATCTGCTGCAGGTT 817
   38 GUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGC 85
  76 AAAAAACUGCAGGACGUU 93
  16 с дес печес по печение по печение по печение по печение по печение по печение печен
   34;
   Similarity
   Similarity
   Andarmani, su
   Stache-Crain, Birgit
   25.8%;
nilarity 54.2%;
Conservative
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CURRENT APPLICATION UNMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/05913
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PRIOR FILING DATE: 1997-09-17
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PRIOR PILING DATE: 1997-09-17
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PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059352
  CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 10/028051
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 08/822333
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1291
  US-10-131-826A-351
Sequence 351, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION
  밁
   В
   Ś
   ; TYPE: DNA
; ORGANISM: Xenopus laevis
US-11-184-005-23
   Ś
   Matches
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  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
  APPLICANT:
  APPLICANT:
   APPLICANT:
  APPLICANT:
  APPLICANT:
   1274 GCTCTTAGCTACATTCAGTCACTGCTCTGTCACTGGAAGTTGATAAACTGCCTGGAACAC 1215
  1214
   61 GUUGAAUGGCUGCGUAAAAACUGCAGGA 89
  1 ecnennocceananocaecomenes de la company de
   36; Conservative
  Similarity 40.4%;
  GTGCAATATAGTTATAAAAAAAAAGAAGGA
   Watanabe, Colin K
Wood, William
  Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
   Gao, Wei-Qiang
Gerritsen, Mary E.
  Beresini, Maureen
DeForge, Laura
  Stewart, Timothy A.
   Sherwood, Steven
   Desnoyers, Luc
Filvaroff, Ellen
   Tumas, Daniel
  Kevin P.
   12;
  Score 23.4; DF Pred. No. 13; 12; Mismatches
  1186
   DB 7;
   41;
  Indels
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   Gaps
  0
```

FILING DATE: 1997-09-19

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; TYPE: DNA; ORGANISM: Homo Sapien US-10-131-826A-351
  RESULT 6
US-10-510-386-67
; Sequence 67, Application US/10510386
; Publication No. US20050244922A1
  S
   밁
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  밁
   გ
   밁
   Ś
  밁
  US-11-033-764-35/c
   RESULT 7
          Sequence 35, Application US/11033764

Publication No. US20050244817A1

GENERAL INFORMATION:
APPLICANT: Rubin, Donald H.
APPLICANT: Organ, Edward L.
APPLICANT: DUBOis, Raymond N.
TITLE OF INVENTION: Mammalian Genes Involved in Viral
TITLE OF INVENTION: Infection and Tumor Suppression
FILE REFERENCE: 01123,0004
   CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 67
SEQ ID NO 67
   SEQ ID NO 351
LENGTH: 4053
  GENERAL INFORMATION:
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   Query Match
   APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
   APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Tro
   Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550
   PRIOR APPLICATION NUMBER: 60/059588 PRIOR FILING DATE: 1997-09-19
CURRENT APPLICATION NUMBER: US/11/033,764
   LENGTH: 2206
TYPE: DNA
ORGANISM: Bacillus licheniformis
FEATURE:
   NAME/KEY: CDS
LOCATION: (501)..(1703)
  y Match 24.9%; Score 23.2; Local Similarity 40.5%; Pred. No. 20;
  Local
   34; Conservative
  619 TTAAAAACAGGCCG 632
   559 TCTGCCTGATGATTGAAGCGGGTGCGGGAATGAACACGACTGAACAGTTTGAGAGCTTAT 618
   14 UCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGC
   10 GAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGG 69
  74 GUAAAAAACUGCAG
   l Similarity
33; Conserv
  GACCATAACAACCTAACAGAGATT 1080
  CUGCGUAAAAAACUGCAGGACGUU 93
   GTAACGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAAATTTTTGCAGCTG 1056
   Jorgensen, Steen Troels
   Conservative
  24.5%;
  87
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   9;
  Score 22.8; Pred. No. 24;
   Mismatches
   DB 1;
   DB 1; Length 2206;
   38;
   32;
   Length 4053;
   Indels
   0,
   Gaps
   0
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   SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 224
LENGTH: 11438
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-224
   밁
   S
   В
   US-11-033-764-35
   CURRENT FILING DATE: 2005-01-12
PRIOR APPLICATION NUMBER: US/10/877,807
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/509,712
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US98/21276
PRIOR APPLICATION NUMBER: PCT/US98/21276
PRIOR FILING DATE: 1998-10-08
PRIOR PFLICATION NUMBER: 60/062,021
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 127
                           Ş
   US-10-821-234-224
   Sequence 224, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 320
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Best Local Similarity
   Matches
   Query Match
   FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
   NUMBER OF SEQ ID NOS: 1704
   APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and
   FEATURE:
NAME/KEY: misc feature
LOCATION: 1-320
OTHER INFORMATION: n =
   TYPE: DNA
ORGANISM: Rattus norvegicus
   / Match 24.1%;
Local Similarity 47.2%;
nes 34; Conservative
   3886 CCAGCTGTGTGCGTGGGCCTCGGCGGCCTCCACTAGACGCAGCTTGCTGCCCGCCGGGG 3945
3946 AGAAGGTCTGCA 3957
   64 AACCAGIGTATACTCTGCCATGGTCCAGGCCTGTACTTCTGTGATCTTGTGTCATGGGTG 5
   13 AUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUG 72
   15 CCAGCUGAUGCACGGUGGUGGUGGUCGGAACCUCCAUGGAACGUGUUGAAUGGCUGCG 74
   73 ÇGUA 76
                                   75 ИАААААСИССА 86
   28;
   4 CATA 1
   Conservative
   24.1%;
   á
   a,
   10;
   Score 22.4; D:
Pred. No. 20;
10; Mismatches
   c or t(u)
   Score 22.4;
Pred. No. 51;
   Mismatches
   DB
   DB 1;
   Treatment of Preeclampsia
   31;
   9;
   26;
   Length 320;
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   Indels
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RESULT 9 US-11-082-389-315

; Sequence 315, Application US/11082389

Publication No. US20050244935A1

```
APPLICANT: Zelder, Uskai
APPLICANT: Laberhauer, Gregor
TITLE OF INVENTION: CORYNBBACTBRUM GLUTAMICUM GENES ENCO
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND N
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-131CPCN
CURRENT FILING DATE: 2005-03-16
PRIOR FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 9/603024
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-07-99
PRIOR FILING DATE: 1999-07-99
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 930487.4
PRIOR APPLICATION NUMBER: DE 1930487.4
PRIOR APPLICATION NUMBER: DE 1930489.0
PRIOR APPLICATION NUMBER: DE 1931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 1931550.7
PRIOR APPLICATION NUMBER: DE 1931550.7
PRIOR APPLICATION NUMBER: DE 1932134.5
PRIOR PILING DATE: 1939-07-09
PRIOR APPLICATION NUMBER: DE 1932134.5
PRIOR APPLICATION N
   RESULT 10
US-11-074-176-353
   밁
   Ś
   US-11-082-389-315
  GENERAL INFORMATION:

APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, william M.
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Oilvia
APPLICANT: McAuliffe, Oilvia
APPLICANT: Petil, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
   Sequence 353, A
Publication No.
  Query Match
Best Local Similarity
  Matches
  APPLICANT:
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version
  FEATURE:
NAME/KEY: CDS
LOCATION: (101)...(1438)
OTHER INFORMATION: RXN01995
   TYPE: DNA ORGANISM: Corynebacterium glutamicum
   1148 GTTGTGGGCATGCTGATCAATGGTTGTGGCTGGTCTGTACACCCTG 1198
   4 GUUUCÇGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUG 54
  23;
  Schroder, Har
Zelder, Oskar
   Application US/11074176
D. US20050250135A1
  23.9%; Score 22.2; ilarity 45.1%; Pred. No. 35; Conservative 10; Mismatches
   Burkhard
   Hartwig
  Mismatches
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   See File Wrapper or PALM
  18;
   Length 1461;
  Indels
   AND MEMBRANE
  o
;
  Gaps
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PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 185
LENGTH: 1224
TYPE: DNA
ORGANISM: Lactobacillus acidophilus
FEATURE:
FEATURE:
  밁
   ; OTHER INFORMATION: ORF 699; phosphoglycerate kinase US-11-074-176-185
  RESULT 11
US-11-074-176-185
   밁
   Ş
  ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 699; phosphoglycerate kinase
US-11-074-176-353
   US-10-793-626-4301/c
  RESULT 12
Sequence 4301, Application US/10793626
Publication No. US2005025478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPPLICOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: US/10/793,626
   Sequence 185, Publication No.
  Matches
  Query Match
Best Local Similarity
   GENERAL INFORMATION:
   Matches
  Query Match
Best Local
  SEQ ID NO 353
   APPLICANT: Altermann, Eric
APPLICANT: McAulife, Olivia
APPLICANT: McAulife, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
  APPLICANT: Klaenhammer, Todd R. APPLICANT: Russell, William M.
  PEATURE: misc_feature
  TYPE: DNA ORGANISM: Lactobacillus acidophilus
  NAME/KEY:
LOCATION:
  FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1209)
   ENGTH:
  1141 GGTGGTGGTTCACTTAACTACCTTGAAGGTAAAGTATTGCCAGGTA 1189
  1156 GGTGGTGGTGCTTCACTTAACTACCTTGAAGGTAAAGTATTGCCAGGTA 1204
   28 ecuecuceuceucucaaacuccauegaaceucuugaauegcueceua 76
   22;
  ch 23.4%; Score 21.8; I Similarity 44.9%; Pred. No. 46; 22; Conservative 10; Mismatches
  1209
  CDS
(1)...(1224)
   Application US/11074176 o. US20050250135A1
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   t; Score 21.8; It; Pred. No. 46; 10; Mismatches
   DB 7; Length 1209;
  DB 7;
  17;
   17;
   Length 1224;
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: nucleic acid sequence US-10-793-626-4301
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US-10-821-234-112
   δ
  밁
  S
  ; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-748
  US-10-821-234-748/c
   밁
   δ
  RESULT 13
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and
FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
   Sequence 112, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
   SOFTWARE: pt_SEQ_genes Version 1.0 SEQ ID NO 748
  Publication No. US2
GENERAL INFORMATION
   Sequence 748, Application US/10821234 Publication No. US20050255114A1
   Query Match 23.4%; Score 21.8; DB 1; Best Local Similarity 44.9%; Pred. No. 56;
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  Matches
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PRIOR FILING DATE: 199-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
  CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
   TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia FILE REFERENCE: 821A
  APPLICANT: Andarmani, APPLICANT: Tang, Y. T
  APPLICANT:
  NUMBER OF SEQ ID NOS: 1704
   APPLICANT: Labat, Ivan
  APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
   ORGANISM: Artificial Sequence FEATURE:
  LENGTH: 2536
TYPE: DNA
  v Match 23.2%; Score 21.6; DB 1; Length 1759;
Local Similarity 44.1%; Pred. No. 60;
nes 30; Conservative 9; Mismatches 29; Indels 0
   1705 TGGTTTTGGTTTCTACTCCAAGAAAGGAATAGCATGACTGATTATGAAA 1657
  469 TTCGCTAGCCTCCTGCAGCGCACCGATGGCTGCGCTCTGAAACCTCAGGTCGGTTTTGAA
  409 ATCCTGCG 402
   33 UGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAA 81
  67
   22;
   7 UCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAA
  ueccuece 74
   Stache-Crain, Birgit
   Conservative
   Susan
   10; Mismatches
   and Treatment of Preeclampsia
   17;
  Length 2536;
   Indels
   0
  0
  Gaps
   Gaps
  410
  66
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   0
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 598
LENGTH: 459
   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-598
  망
  ; TYPE: DNA; ORGANISM: Homo sapiens US-10-821-234-112
Search completed: November 24, 2005, 04:56:47 Job time : 195 secs
   밁
   Ş
   RESULT 15
US-10-821-234-598
   밁
   ঠ
   Ś
  Sequence 598, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
   NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 112
LENGTH: 3901
   Query Match
Best Local Similarity
Matches 30; Conserv
   Matches
  Query Match
Best Local
   APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
  FILE REFERENCE: 821A
  Local Similarity
   2374 TCCAGGTGATCCATCCTTGCCATCTTCGCCTTTAGCTCCTGGAACACCTGGAATACCAGC 2433
   2434 CTCACCGCGTTCACCACGT 2452
   14 UCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGC 73
   74 GUAAAAACUGCAGGACGU 92
   17 TCCTGCTGAAGCCCTGGTGGGGAGGGGGACAGAGCGAGATGGGGGCGTAATGGAATGCT 74
   14 UCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCU 71
   29;
  Conservative 13; Mismatches
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  22.8%;
   23.0%; Score 21.4; 38.0%; Pred. No. 87;
   6;
   Score 21.2; Di
Pred. No. 58;
6; Mismatches
  DB 1;
   DB 1;
  36;
   23;
  Length 3901;
   Length 459;
   Indels
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  Gaps
   Gaps
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Maximum DB seq length: 200000000
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  Database
   Post-processing:
  Total number of hits satisfying chosen parameters:
  Searched:
  Scoring table:
   Sequence:
  Perfect score:
   Run on:
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  N_Geneseq_21:*
1: geneseqn1980
2: geneseqn2900
3: geneseqn2001
4: geneseqn2001
5: geneseqn2002
7: geneseqn2002
7: geneseqn2003
10: geneseqn200
11: geneseqn200
11: geneseqn200
13: geneseqn200
14: geneseqn200
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Gapop 10.0 , Gapext 1.0
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93
  November 23, 2005, 22:00:32; Search time 242.667 Seconds (without alignments) 2554.189 Million cell updates/sec
  4996997 seqs, 3332346308 residues
   1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93
   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqn2002bs:*
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: geneseqn2004bs:*
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   geneseqn1990s:*
  geneseqn1980s:*
   9993994
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ALIGNMENTS

| 13        |        | 18                 | 17                 | 16                | 15                 | 14                 | 13                 | 12                 | 11                 | 10                 | 9        | 8                  | 7                  | 6                  | <b>σ</b> | 4                  | ω                  | N                  | <b>-</b>           | Result<br>No. |   |
|-----------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|---------------|---|
| 9         |        | 60                 | 60                 | 60                | 60                 | 60                 | 60                 | 60                 | 60                 | 60                 | 60       | 60                 | 60                 | 60                 | 60       | 61.6               | 64.2               | 83.4               | 93                 | Score         |   |
| 01.0      |        | 64.5               | 64.5               | 64.5              | 64.5               | 64.5               | 64.5               | 64.5               | 64.5               | 64.5               | 64.5     | 64.5               | 64.5               | 64.5               | 64.5     | 66.2               | 69.0               | 89.7               | 100.0              | Query         | ф |
| 202       | 3 (    | 276                | 276                | 276               | 264                | 252                | 252                | 168                | 117                | 111                | 111      | 111                | 102                | 102                | 102      | 152                | 93                 | 93                 | 93                 | Length        |   |
| -         |        | 12                 | 12                 | 12                | 12                 | 12                 | 12                 | N                  | 12                 | 13                 | 12       | 12                 | 13                 | 12                 | 12       | N                  | w                  | ω                  | ω                  | В             |   |
| VICTOR OF | 200000 | ADJ87051           | ADJ65899           | ADF90345          | ADJ65913           | ADJ65859           | ADG93181           | AAT34865           | ADG93260           | ADW14375           | ADJ65858 | ADG93180           | ADW14377           | ADJ65857           | ADG93179 | AAT73910           | AAA51731           | AAA51729           | AAA51730           | ĬD            |   |
|           | •      | Adj87051 Nucleotid | Adj65899 PTH DNA s | Adf90345 Chimeric | Adj65913 Tandem po | Adj65859 PTH prote | Adg93181 Novel exp | Aat34865 Plasmid p | Adg93260 Novel exp | Adw14375 Human par |          | Adg93180 Novel exp | Adw14377 Human par | Adj65857 PTH pepti | _        | Aat73910 Synthetic | Aaa51731 PTH funct | Aaa51729 PTH funct | Aaa51730 PTH funct | Description   |   |

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

| 45        | 44        | 43        | 42        | 41        | 40        | 39        | 38        | 37       | 36       | 35          | 34       | 33       | 32       | 31       | 30       | 29       | 28       | 27       | 26       | 25       | 24       | 23       | 22       | 21       | 0.2    |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|----------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--------|
| 50.4      | 50.4      | 50.4      | 50.4      | 50.4      | 50.4      | 50.4      | 50.4      | 51       | 51       | 52.6        | 54.2     | 54.2     | 54.2     | 58.4     | 58.4     | 58.4     | 58.4     | 58.4     | 60       | 60       | 60       | 60       | 60       | 60       | đ      |
|           |           |           |           | 54.2      |           |           |           |          |          |             |          | •        |          | •        |          | ٠        | ٠        | 62.8     |          | ٠        |          | ٠        | •        | 64.5     | ٠      |
| 435       | 423       | 417       | 414       | 411       | 408       | 408       | 405       | 945      | 728      | 145         | 207      | 141      | 141      | 489      | 489      | 489      | 114      | 108      | 528      | 426      | 420      | 321      | 294      | 291      | 167    |
| ω         | w         | w         | w         | w         | w         | w         | w         | N        | N        | 13          | 2        | N        | N        | 12       | 12       | 12       | 13       | 13       | σ        | 12       | 12       | 12       | 2        | 12       | 7.1    |
| AAA51458  | AAA51457  | AAA51456  | AAA51459  | AAA51453  | AAA51454  | AAA51455  | AAA51452  | AAQ55302 | AAQ55301 | ADW80822    | AAQ89923 | AAT80383 | AAQ89920 | ADG68786 | ADG48059 | ADG48030 | ADV69502 | ADV69494 | AAS19702 | ADF90347 | ADJ65917 | ADJ65915 | AAT34866 | ADJ65900 | 200000 |
| Aaa51458  | Aaa51457  | Aaa51456  | Aaa51459  | Aaa51453  | Aaa51454  | Aaa51455  | Aaa51452  | Aaq55302 | Aaq55301 | Adw80822    | Aaq89923 | Aat80383 | Aaq89920 | Adg68786 | Adg48059 | Adg48030 | Adv69502 | Adv69494 | Aas19702 | Ad£90347 | Adj65917 | Adjesyls | Aacsass  | Adjesyou | 10000  |
| PCpB-DFIA | PCDR-DOVD | PCDB-VIPR | PCpB-APK- | PCpB-ALY- | PCDB-TECK | PCpB-LVPR | PCpB-RVR- |          |          | 2 DNA encod | Taker    |          |          | σ        |          | Human    |          | Human    | _        | -        |          | Tandem   | Plasmid  | PIH DNA  |        |

#### RESULT 1 AAA51730 Homo sapiens. Synthetic. AAA51730; AAA51730 standard; RNA; 93 BP PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss. PTH functional domain conjugate peptide PG7 coding sequence. 31-OCT-2000 WPI; 2000-452384/39. P-PSDB; AAY96975. Gardella TJ, Kronenberg HM, (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M. (POTT/) POTTS J T. (JUEP/) JUEPPNER H. 31-DEC-1998; 30-DEC-1999; 06-JUL-2000. WO200039278-A2 (first entry) 98US-0114577P 99WO-US031108. Location/Qualifiers /\*tag= a /product= "PG7" Potts JT, Jueppner H;

Claim 14; Fig 1; 119pp; English

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   á
   Matches
  Query Match
Best Local
  Compounds of the structure or formula S-(L)_n-B, R 1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of pTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence; are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inhalation unlike the large native PTH or PTH-rP which avoids the need for regular injections to treat osteoporosis
                        WPI; 2000-452384/39
P-PSDB; AAY96973.
   (GARD/)
(KRON/)
(POTT/)
(JUEP/)
New compound comprising
  30-DEC-1999;
  PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss.
   Sequence 93
  31-DEC-1998;
  WO200039278-A2.
  Synthetic.
   PTH functional domain conjugate peptide PG5 coding sequence.
   31-OCT-2000
  AAA51729 standard; RNA;
   sapiens
  13
  61
   ) GARDELLA T J.
) KRONENBERG H M.
) POTTS J T.
) JUEPPNER H.
   1
   1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGCCAUGGAACGU
   l Similarity
93; Conserv
   ij
  GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU
  GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
   Conservative
  BP; 19 A; 16 C; 33 G; 0 T; 25
   (first entry)
   Kronenberg
  98US-0114577P
   99WO-US031108
   Location/Qualifiers
   /*tag= a
/product= "PG5"
  100.0%;
   93
 an
   Ĭ,
amino terminal signaling functional domain
  ΒP
   0;
   Score 93; DB 3;
Pred. No. 3.7e-20;
   Potts
   Mismatches
   JT,
   U; 0 Other;
  <u>,,</u>
   Length
   Indels
  93;
   0,
   Gaps
   60
  60
   0,
```

```
linked to a carboxy-terminal binding portion of parathyroid treating mammalian conditions characterized by decreases in
  Claim 14;
  Fig 1; 119pp; English.
   hormone for bone mass.
```

Compounds of the structure or formula S-(L)\_n-B, R-1-S-(L)\_n-R or S-(L)\_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PPH), L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PPH(1-34) or a PTH-related protein (PPH-rP) (1-34); R 1 is the requence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis

```
RESULT 3
AAA5171
ID AAA5
XX AAA517
AAC AAA5
XX PTH
XX PT
XX HOMO
OS Syntt
XX WO20
XX WO11
XX GARD
A (GARD
A (GAR
  밁
   Ş
   밁
  Ś
   Query Match
Best Local S
Matches 87
  Homo sapiens.
Synthetic.
   31-OCT-2000
  AAA51731;
   (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
  31-DEC-1998;
   30-DEC-1999;
  06-JUL-2000.
   WO200039278-A2
  PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss.
   PTH functional domain conjugate peptide PG9 coding sequence.
  AAA51731 standard; RNA;
  Sequence
   61
  61
  ь
   l Similarity
87; Conserv
   GCUGUUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU
  93
   GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGU
  BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;
   Conservative
   (first entry)
   98US-0114577P
   99WO-US031108
  Location/Qualifiers
   /*tag= a
/product= "PG9"
  89.7%;
   93
  ВP
  Score 83.4; D
Pred. No. 4.6e
0; Mismatches
   0,
  DB 3; Length 93; .6e-17;
  93
  93
   0;
   Gaps
  60
   60
   0
```

WPI; 2000-452384/39 P-PSDB; AAY96974.

Gardella TJ,

Kronenberg

Ĭ,

Potts ŢŢ,

Jueppner

H

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RESULT 4
AA773 01
ID AA777
XX
AA778 01

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  Matches
   Query Match
Best Local (
   Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for
   New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   Synthetic
  Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; endoproteinase LysC; ds.
   Synthetic oligonucleotide encoding linker and PTH 1-37.
   25-MAR-2003
30-JAN-1998
  AAT73910;
  Sequence 93
  Claim 14; Fig 1; 119pp; English.
   misc_feature
   Homo
   AAT73910 standard; DNA; 152 BP.
  16-NOV-1995;
   06-NOV-1996;
   22-MAY-1997.
  WO9718314-A1
                                  (BOEF )
   sapiens.
  61
  13
   75;
  ب
  Similarity
                                  BOEHRINGER MANNHEIM GMBH
  injections to treat osteoporosis
  GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGU 60
   GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
  GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;
  Conservative
  (first entry)
   (revised)
  95DE-01042702.
   96WO-EP004850
   of present
  Location/Qualifiers
   . 152
   69.0%;
   Ω.
  end_of complementary strand overhangs 3'
strand by sequence 5'-TCGA-3'"
   Score 64.2; DB 3;
Pred. No. 7e-11;
0; Mismatches 18;
  93
  18; Indels
   Length
   0;
  Gaps
  0
```

```
ADG93179
ADG93179
ADG93179
ADG93179
AC ADG9
XX ADG9
XX ADG9
XX ADG9
XX Hove
XX Expr
KW Expr
KW Expr
KW Expr
KW W020
XX Unid
XX
  밁
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  밁
  Ś
   The present sequence, which encodes a linker and the parathyroid hormone CC 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was CC ligated to the 2.9 kb Nhel-HindIII fragment of pSAM-CORE, which contains CC the Met(13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-CC PTH and the LacIq repressor plasmid pUBS500 were used to transform E. CC coli K12 RM82. The transformants were grown, with IPTG induction, in CC medium containing kanamycin and ampilcilin. Cells were harvested, lysed CC and isolated inclusion bodies solubilised in guanidine hydrochloride, and CC renatured by dilution in pH 7 phosphate buffer. The solution was CC larified and the supernatant concentrated and purified on a column of CC immobilised iminobiotin. The purified material was incubated with CC endoproteinase LysC and the PTH 1-37 fragment released, recovered by SA CC fragment removal on an iminobiotin column followed by chromatography on a CC fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the CC finker, i.e. nor tailvay residues in SA (Indated and SK-MAB-2001 to the Lys residue in CC the linker, i.e. nor tailvay residues in SA (Indated and SK-MAB-2001 to CC the linker, i.e. nor tailvay residues in SA (Indated and SK-MAB-2001 to CC the linker).
  Matches
   Query Match
   Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and parathyroid
  Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;
   Example 2; Fig 2; 37pp;
  hormone production.
   P-PSDB; AAW21946
   WPI; 1997-289290/26
  Kopetzki E;
WPI; 2004-035128/03
   expression cassette; high yield polypeptide production tandem polypeptide; inclusion body; gene; ds.
  correct PR field.)
   Harley S,
   23-MAY-2003; 2003WO-US016643
  04-DEC-2003
  WO2003100021-A2
  Unidentified
  Novel expression cassette-related polypeptide-encoding DNA SeqID60
   11-MAR-2004 (first entry)
   ADG93179 standard; DNA; 102 BP
  24-MAY-2002; 2002US-0383370F
  (REST-) RESTORAGEN INC
  Local Similarity
  97
   37
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  55,
   N
  cuguruccgaaauccagcugaugcacgguggugguggugguggugguuccauggaacgug 61
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128
   Williams JA,
   Conservative
   not at Lys residues in SA. (Updated on
  66.2%;
59.8%;
  German.
   Luan P,
  18:
  Score 61.6;
Pred. No. 5.
  Mismatches
  Xia Y;
  6; DB 2;
5.4e-10;
   93
  Length 152;
   Indels
  25-MAR-2003 to
  0
  Gaps
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SXCCCCCCCCX SX THIX
  Ş
  밁
  Ś
  Query Match
Best Local S
Matches 53
  This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide polypeptide in a cell, preferably a tandem polypeptide that forms an
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  Disclosure; SEQ ID
  24-MAY-2002; 2002US-0383212P
  23-MAY-2003; 2003WO-US016645
   WO2003100022-A2
   expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
  PTH peptide coding sequence
  06-MAY-2004
   ADJ65857;
   ADJ65857
   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;
  Disclosure; SEQ ID NO 60; 157pp; English.
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  (REST-)
   2004-035129/03
DB; ADJ65837.
  53;
   62 TIGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGGAACGUG 61
   2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   Similarity
  RESTORAGEN
   standard;
   Conservative
  (first entry)
   DNA;
  NO 33; 132pp; English.
  INC
   64.5%;
   19;
  #1
  Score 60; DB 12; I
Pred. No. 1.6e-09;
P; Mismatches 20;
   93
  Length 102;
   Indels
  0;
  61
   0
  AND ALTER AND AL
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  ព្រព្ពន្ធន
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   Query Match
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Matches 53
   Query Match
Best Local S
Matches 53
   18-JUN-2003.
  Homo
   ADW14377;
   10-MAR-2005
  (SHAN-)
   ú
  sapiens
  62
   62
  62
   Ν
   N
  N
   N
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
```

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62

TTGAATGGCTGCGTAAAAAACTGCAGGACGTT

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The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADM14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADM14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the PTH 1-34 peptide.
  Sequence 102 BP;
  inclusion body when a peptide which may of the invention.
   Sequence 102 BP;
   Human parathyroxin PTH 1-34 peptide encoding
  Disclosure; SEQ ID NO
   Production of reorganized human parathyroid hormone 1-34 peptide.
  ADW14377 standard;
  12-DEC-2001; 2001CN-00142627
   12-DEC-2001;
  parathyroxin;
  2004-099606/11.
DB; ADW14378.
   l Similarity
53; Conserv
   l Similarity
53; Conser
   SHANGHAI BIOLOGICAL
  Xiu C,
UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
   64.5%;
llarity 57.6%;
Conservative 1
   Conservative
   2001CN-00142627
  Ľ
  30 A; 24 C;
   30 A; 24 C; 22 G;
  recombinant
  DNA;
  3
   expressed in a be used in the
   64.5%;
  3; 25pp; Chinese.
  102
  19;
   19;
  Score 60; DB
Pred. No. 1.6e
19; Mismatches
  ENG
   Score 60; DB
Pred. No. 1.6e
19; Mismatches
  ВÞ
  22 G;
  protein;
  RES
   cell. The present DNA sequence encodes construction of a tandem polypeptide
   26 T; 0 U; 0 Other;
  26 T; 0 U; 0
  CENT
   1.6e-09;
ches 20;
  protein engineering
  DB 13;
   DB 12;
  .6e-09;
les 20;
  ACAD
   DNA SEQ ID NO:3
  Length 102;
  Length 102;
  Other;
  0
   0,
   Gaps
  Gaps
   61
                              61
  61
   61
   0
```

```
RESULT 8
ADG93180
RESULT 9
ADJ65858
ID ADJ6
XX
AC ADJ6
AC ADD7
AC ADD7
AC ADD7
AC ADD7
AC ADD7
AC ADT7
A
  밁
   δ
  밁
   á
  Query Match
Best Local :
  Matches
   This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
  Harley S,
   04-DEC-2003
  expression cassette; high yield polypeptide production;
   Novel expression cassette-related polypeptide-encoding DNA SeqID61.
  11-MAR-2004
  ADG93180 standard;
   Disclosure; SEQ ID NO 61; 157pp; English.
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   WPI; 2004-035128/03
  24-MAY-2002; 2002US-0383370P
  23-MAY-2003; 2003WO-US016643
   WO2003100021-A2
  06-MAY-2004
   ADJ65858 standard; DNA; 111 BP
  Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
                       peptide
  62
   62
  polypeptide;
   N
  53;
  N
  Similarity
  RESTORAGEN INC
  UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
   Williams
                            coding
   Conservative
  (first
  (first entry)
                            sequence #2
  JA,
   inclusion body; gene; ds
  64.5%; Score 60; 57.6%; Pred. No.
   Luan
   19;
  ש
  Mismatches
   Xia
  1.6e-09;
   DB 12;
   20;
   Length 111;
   Indels
   0
   Gaps
  61
  61
```

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RESULT 10
ADW14375
   Ś
  밁
   Ş
Query Match
Best Local s
  Matches
  The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
  expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   23-MAY-2003; 2003WO-US016645
  04-DEC-2003
   WO2003100022-A2
   Disclosure; SEQ ID NO 34; 132pp; English.
   24-MAY-2002; 2002US-0383212P
  CN1424325-A.
  Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID
  10-MAR-2005
  ADW14375
   Sequence 111 BP;
   WPI; 2004-035129/03.
P-PSDB; ADJ65838.
  (REST-) RESTORAGEN
  12-DEC-2001; 2001CN-00142627.
  12-DEC-2001; 2001CN-00142627
   Homo sapiens
                            (SHAN-) SHANGHAI BIOLOGICAL ENG
   L8-JUN-2003
   ocal Similarity
  parathyroxin;
   62
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  53;
   N
  2 сидиписсерала иссъества иссъествение в предоставления в
   Peng L;
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
  standard; DNA; 111 BP
  Conservative
   30 A; 26 C;
   recombinant protein; protein engineering
  INC
  64.5%;
   19;
   Score 60; DB 12, Pred. No. 1.6e-09;
   25 G; 30 T; 0 U; 0 Other;
                               RES
                               CENT ACAD
   93
   Length 111,
  Indels
  0;
  Gaps
  61
```

```
RESULT 11
ADG93260
밁
  ş
  В
  Ś
  Query Ma
Best Loc
Matches
  The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the Gly-Ser-Pro-PTH 1-34 peptide.
  New expression cassette comprising an operably linked nucleic sequence, useful for producing a tandem polypeptide that forms inclusion body when expressed in a cell.
  Chen
  04-DEC-2003
  Synthetic
  expression cassette;
tandem polypeptide;
   Sequence 111 BP; 31
  Claim 3; SEQ
   Disclosure;
  Harley
  (HARL/)
   24-MAY-2002; 2002US-0383370P
   23-MAY-2003; 2003WO-US016643
  WO2003100021-A2
   Unidentified
  Novel expression cassette-related
  ADG93260
  Production of reorganized human parathyroid
  Match
  2004-099606/11.
DB; ADW14376.
   ņ
  2004-035128/03
DB; ADG93259.
  71
  62
  11
  Ś
  N
   53;
  RESTORAGEN INC
HARLEY S.
  Similarity
  Xiu
   TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
   CUGUUUGGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGGUGGAACGUG
   standard;
  Williams
   Conservative
  ú
   ID NO 1; 25pp; Chinese.
   (first
   Ħ
   Ε.
   ö
   DNA;
  A; 28 C;
  3
  high yield polypeptide production; inclusion body; gene; ds; PTH.
  entry)
  64.5%;
57.6%;
   141; 157pp;
  117
  Luan
   ВP
  Score
Pred.
   25 G;
  ,
   Mismatches
  PTH DNA SeqID141
  English.
   Xia
  NO.
  27
  T; 0 U; 0 Other;
  DB 13;
  6e-09;
  hormone
   20;
  Length
  1 - 34
  peptide
   Gaps
  70
  61
   0
```

This invention relates to a novel expression cassette and methods in this pield production of polypeptides. The cassette comprises an oplinked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expension of the cassette produces a tandem polypeptide that forms an inclusion body when expensions are the produces at an acid sequence.

expressed

Sequence

168

BP;

41

A.

44 C;

42

G;

41

Ή.

0 U;

Other;

operably 101

```
AAT34865
ID AAT34
ACC
XX AAT34
ACC
XX P1Asm
XX PTH;
KW PTH;
KW Vecto
OS Synth
XX VECTO
OS SYNTH
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   Query Match
Best Local S
Matches 53
  and transpeptidation of r constructs.
   A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding for a fusion protein (AAR87867) composed of the C-terminal end of human carbonic anhydrase II joined by an intraconnecting peptide (including a thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in E. coli transformants. The intraconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be selectively reacted to produce C-terminal carboxamidated PTH(1-34)
   in a cell. The expression cassette is useful for producing peptide polypeptide in a cell, preferably a tandem polypeptide that forms a inclusion body when expressed in a cell. The present sequence is the a DNA sequence which encodes a PTH peptide which was used in the exemplification of the invention.
  WPI; 1996-287185/29.
P-PSDB; AAR98967.
  Sequence 117 BP; 35 A; 27 C; 25 G;
   Example 7; Fig 1; 93pp; English.
   07-DEC-1994;
  07-DEC-1995;
   13-JUN-1996.
   Synthetic.
   vector; plasmid
  Plasmid
  02-DEC-1996
  AAT34865;
  AAT34865
   (BION-) BIONEBRASKA
   IH; parathyroid hormone; parathormone; (lpha-carboxamide; recombinant protein; lector; plasmid pBNI; carbonic anhydrase
  JS,
   62
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  l Similarity
53; Conserv
   N
   N
  PBN1:PTH(1-34)C-1c
  standard;
   cugurucceaaauccaecueauecacecueeueeueeueeueeueeuuccaueeaaceue
   Patridge
   64.5%;
ilarity 57.6%;
Conservative 1
  (first
   94US-00350528
  95WO-US015799
   Location/Qualifiers
   /*tag= a
/product= "hCA-linker-PTH(1-34)Cys
  cDNA;
  BE,
   entry)
  l alpha-carboxamidated recombinant multicopy
  168
  Heriksen
  %; Score 60; DB
%; Pred. No. 1.76
19; Mismatches
  portion encoding
  ВP
  B,
   30 T; 0 U; 0
  Holmquist
  C-amide; C-amidated peptide;
fusion protein; transpeptidation;
e II; ss.
   DB 12;
  7e-09;
  93
  93
  PTH (1-34) Cys.
   peptide(s)
   Length 117;
  Other;
  ä
  fusion"
  Wagner
   g i
   by cleavage
r fusion
   0
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   and
   61
  of.
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RESULT 13
ADG93181
  밁
  δ
   밁
   5
             δ
   뭐
   δ
  Query Match
Best Local Similarity
   Matches
  Query Match
Best Local
   This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  Disclosure; SEQ ID NO 62; 157pp; English.
   04-DEC-2003.
  WO2003100021-A2
   tandem
   Novel expression cassette-related polypeptide-encoding DNA SeqID62.
  Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
   WPI; 2004-035128/03.
  Harley S,
   24-MAY-2002; 2002US-0383370P
   23-MAY-2003; 2003WO-US016643.
  Unidentified
   expression cassette;
   ADG93181 standard; DNA; 252
   (REST-)
  Local Similarity
  107
  47
62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:||||:::
   53;
  53
  polypeptide;
  N
  N
   RESTORAGEN INC
HARLEY S.
  ADG93161
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 106
  CUGUUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
  TTGAATGGCTGCGTAAAAACTGCAGGACGTT 138
   CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
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  Williams
   Conservative
  Conservative
   (first entry)
  JA,
  ; high yield polypeptide production; inclusion body; gene; ds.
  64.5%;
57.6%;
   64.5%;
57.6%;
  Luan
   19;
  ; Score 60; DB 12; Length 25; Pred. No. 2e-09; 19; Mismatches 20; Indels
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Pred. No. 1.8e-09;
L9; Mismatches 20
  Ψ,
  Xia
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   Length 252;
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   Gaps
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  13
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   0
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RESULT 14
ADJ659
ADJ659
ADJ659
AC ADJ66
ADJ65913
ID ADJ659
XX ADJ65
XX ADJ65
XX ADJ65
XX O6-MA
XX Tande
XX Tande
XX Expre
   밁
  밁
   á
  밁
   8
  Matches
  Query Match
   polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a protein which may be used in the construction of a tandem polypeptide of the invention.
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
   06-MAY-2004
   ADJ65859;
  ADJ65859
  Tandem polypeptide-encoding
  Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
   04-DEC-2003.
  expression cassette; tandem polypeptide; inclusion body;
   06-MAY-2004
   ADJ65913
  ADJ65913 standard; DNA;
   The invention comprises an expression cassette which produces a tandem
   Disclosure; SEQ ID NO 35; 132pp; English.
   P-PSDB;
   WPI; 2004-035129/03.
   Xia Y,
   24-MAY-2002; 2002US-0383212P
   23-MAY-2003; 2003WO-US016645
   WO2003100022-A2
   Unidentified
  PTH protein coding sequence
  Local Similarity es 53; Conserv
   62
  62
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  N
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
   ADJ65839.
  Peng L;
   RESTORAGEN
   standard; DNA;
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
  TTGAATGGCTGCGTAAAAACTGCAGGACGTT
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   64.5%;
milarity 57.6%;
Conservative 19
   (first entry)
   (first entry)
   264
   252 BP
  19;
   ВP
  expression cassette #6
  Score 60;
Pred. No.
   Mismatches
   No.
  2e-09;
  DB 12;
  93
   20;
  Length 252;
   Indels
   ,
,
   Gaps
  61
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Search completed: November 23, 2005, 23:00:14 Job time: 242.667 secs
  유양
  D<sub>P</sub>
   Ş
   Query Match
Best Local S
Matches 53
  The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence represents an expression cassette which encodes a tandem polypeptide of the invention.
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
  Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;
   WPI; 2004-035129/03.
P-PSDB; ADJ65912.
   Unidentified
   Disclosure; SEQ ID NO 89; 132pp; English.
   Хiа Y,
  24-MAY-2002; 2002US-0383212P
   23-MAY-2003; 2003WO-US016645.
  04-DEC-2003.
  WO2003100022-A2.
   (REST-)
  inclusion body fusion partner;
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||||::
65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96
   ch 64.5%; Score 60; DB 12; Length 264; I Similarity 57.6%; Pred. No. 2e-09; 53; Conservative 19; Mismatches 20; Indels
   Peng L;
   RESTORAGEN INC.
  gene; ds.
   0,
   Gaps
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No.
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
  Total number of hits satisfying chosen parameters:
   Searched:
   Scoring table:
   Sequence:
   Title:
Perfect score:
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  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
   GenEmbl:*

1: gb_ba:*
2: gb_in:*
3: gb_env
4: gb_ow
6: gb_pc
7: gb_p
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10: gb
11: g
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   US-09-475-158A-15
93
   5883141 seqs, 28421725653 residues
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   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
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9b env: *
9b env: *
9b pat:  Length DB
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93
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AR17779
AR17780
AR043797
A36847
A36847
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  11766282
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BD266832 PTH funct
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AR005133 Sequence
AR17779 Sequence
AR17779 Sequence
AR17779 Sequence
AR177780 Sequence
AR17780 Sequence
AR643797 Sequence
AR6437 Sequence
AR6437 Sequence
BD234385 Recombina
BD234386 Recombina
BD234386 Recombina
BD234386 Recombina
BD234380 Recombina
BD234380 Recombina
BD234380 Recombina
   Description
  93
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| 45                | 44                 | 43       | 42                 | 41       | 40       | 39       | 38                |                   |                   | c 35               |                   | 33                 | 32                | 31     | 30     | 29                | 28                | 27     | 26     | 25                | 24       | 23                | 22       | 21                 | 20                | 19                 |
|-------------------|--------------------|----------|--------------------|----------|----------|----------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------|--------|-------------------|-------------------|--------|--------|-------------------|----------|-------------------|----------|--------------------|-------------------|--------------------|
| 43                | 43                 | 43       | 43                 | 43       | 43       | 43       | 43                | 43.4              | 44.6              | 44.6               | 44.6              | 44.6               | 44.6              | 44.6   | 44.6   | 44.6              | 44.6              | 44.6   | 44.6   | 44.6              | 44.6     | 44.6              | 44.6     | 46.2               | 46.2              | 50.4               |
| 46.2              | 46.2               | 46.2     | 46.2               | 46.2     | 46.2     | 46.2     | 46.2              | 46.7              | 48.0              | 48.0               | 48.0              | 48.0               | 48.0              | 48.0   | 48.0   | 48.0              | 48.0              | 48.0   | 48.0   | 48.0              |          | 48.0              | 48.0     | 49.7               | 49.7              | 54.2               |
| 252               | 240                | 225      | 201                | 186      | 102      | 67       | 67                | 74                | 265               | 265                | 265               | 263                | 263               | 263    | 263    | 263               | 252               | 252    | 252    | 252               | 252      | 252               | 252      | 252                | 252               | 435                |
| Q                 | σ                  | σ        | σ                  | თ        | σ        | თ        | δ                 | 9                 | σ                 | σ                  | σ                 | 1                  | 6                 | δ      | δ      | 6                 | 6                 | σ      | σ      | σ                 | σ        | σ                 | σ        | σ                  | σ                 | σ                  |
| AR027050          | BD170198           | BD170211 | BD170213           | BD170222 | BD170195 | AR135774 | A79761            | AR043802          | I83596            | 臣05672             | AR027021          | S71759             | I83595            | E05671 | E04335 | AR027020          | I83594            | E05673 | E05658 | AR168173          | AR030635 | AR027044          | AR027011 | E05675             | AR027046          | BD234389           |
| AR027050 Sequence | BD170198 Process f | Process  | BD170213 Process t | Process  | Process  | Sequence | A79761 Sequence 9 | AR043802 Sequence | 183596 Sequence 4 | E05672 DNA encodin | AR027021 Sequence | S71759 human parat | I83595 Sequence 3 |        |        | AR027020 Sequence | I83594 Sequence 1 |        |        | AR168173 Sequence |          | AR027044 Sequence |          | E05675 DNA encodin | AR027046 Sequence | BD234389 Recombina |

## ALIGNMENTS

| Query Match                           | FEATURES<br>SOUTCE<br>ORIGIN                                                                                                                             |                                                                                                                                                                              | COMMENT:                                                                                                                      | ORGANISM REFERENCE AUTHORS TITLE JOURNAL | RESULT 1 BD266833 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE                                                                                                                                       |
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| ch 100.0%; Score 93; DB 6; Length 93; | FT source 193 FT /organism='Artificial Sequence'. Location/Qualifiers 193 /organism="synthetic construct" /mol_type="genomic RNA" /db_xref="taxon:32630" | THOMAS J GARDELL<br>EPPNER C12N15/09, A61K38<br>A61P19/10,<br>A61P43/00, C07K14<br>A61P43/10, G01N33/<br>C12N1/21,<br>C12N5/10, G01N33/<br>BCription of Artifi<br>Location/Q | AFTILICIAL Sequence JP 2002533115-A/2 08-OCT-2002 30-DEC-1999 JP 2000591171 31-DEC-1998 US 60/114577 31-DEC-1998 US 60/114577 | rder<br>ten                              | BD266833  BD266833  PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.  BD266833  BD266833.1 GI:33076601  JP 2002533115-A/2.  synthetic construct |

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ACCESSION
VERSION
KEYWORDS
  RESULT 3
BD266834
LOCUS
DEFINITION
   REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
   ACCESSION
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   В
  DEFINITION
  FEATURES
   Query Match
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Matches 64
  Matches
  JOURNAL
  PIH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
Patent: up 2002533115-A 1 08-OCT-2002;
INT OS Artificial Sequence PN JP 2002533115-A/1
PD 08-OCT-2002
PF 30-DEC-1909 JP 2007
PR 31-DEC-1909 JP 2007
PR 31-DEC-1909 JP 2007
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Location/Qualifiers
  JUEPPNER
PC C12
  1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUCCAUGGAACGU
                                       BD266834 93 bp RNA linear PAT 17-JUL-2003 PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.
BD266834
   μ
  بر
   64;
    BD266834.1 GI:33076602
JP 2002533115-A/3.
   ŦŦ
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93 bp RNA
PTH functional domain conjugate peptides,
novel tethered ligand-receptor molecules.
   Similarity
  GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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JOURNAL
  RESULT 4
AR269042
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  source
  source
   synthetic construct

Synthetic construct

other sequences, artificial sequences.

1 (bases 1 to 93)

RS Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H.

RS FTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

novel tethered ligand-receptor molecules

novel tethered ligand-receptor molecules

Patent: JP 2002533115-A, 3 08-OCT-2002;

THE GENERAL HOSPITAL CORP

OS Artificial Sequence

PN JP 2002533115-A, 3

PD 08-OCT-2002

PN 08-OCT-2002

PN 30-DEC-1998 US 60/114577

PR 31-DEC-1998 US 60/114577
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  61
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Description of Artificial Sequence: modified PTH sequence FH
   1 (bases 1 to 258)
Jung,E.-K., Park,D.-H. and Chung,S.-I.
Jung,E.-K., Park,D.-H. and Chung,S.-I.
Recombinant expression vector of human parathyroid hormone
Patent: US 6500647-A 26 31-DEC-2002;
Mogam Biotechnology Research Institute; Kyonggi-Do;
KRX;
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Sequence 26 from patent
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LOCUS
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KEYWORDS
SOURCE
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  1 (bases 1 to 141)
Holladay,L.A. and Oldenburg,K.R.
Method for increasing the electrotransport
Patent: US 5747453-A 5 05-MAY-1998;
Location/Qualifiers
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Holladay, L.A. and Oldenburg, K.R.
Method for increasing the electrotransport
Patent: US 5747453-A 3 05-MAY-1998;
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AR043797
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ACCESSION
VERSION
  RESULT 8
AR177780/c
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Holladay,L.A. and Oldenburg,K.R.
Method for increasing the electrotransport
Patent: US 6313092-A 5 06-NOV-2001;
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   1 (bases 1 to 141)
Holladay, L.A. and Oldenburg, K.R.
Method for increasing the electrotransport flux of polypeptides
Patent: US 6313092-A 3 06-NOV-2001;
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Unclassified.

ORS Oldenburg, K.R. and Selick, H.E.

Compounds with PTH activity

RNAL Patent: US 5814603-A 29-58P-1998,
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E 1 (bases 1 to 717)

B Bauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gra Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Patent: WO 9403510-A 1 03-FEB-1994;

SANDOZ AG (AT)

Other publication CZ 950008 951018

Other publication CZ 950008 951018

Other publication SW 4156693 940120

Other publication SW 248137 951221

Other publication WZ 248137 951221

Other publication CR 2260176 940202

Other publication CR 2100423 940705

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Other publication DE 4393381T 950427

Other publication DE 3905126 950116

Other publication FI 950171 950313.
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|                                            | Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92 :    :   :   :     :     :     :     :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| GGAACGUG 61<br>      : <br>CGAGCGTG 130    | SOURCE unidentified SOURCE unidentified unclassified sequences.  REFERENCE 1 (bases 1 to 945)  AUTHORS Bauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gram, H., Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Lewis, I.  TITLE ANALOSS OF PTH JOURNAL Patent: WO 9402510-A 3 03-FEB-1994;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| T 05-MAR-1997                              | COMMENT Other publication HU 70459 951030 Other publication C 9500088 951018 Other publication AU 4156693 940120 Other publication SK 4395 950607 Other publication SK 4395 950607 Other publication SK 248137 951221 Other publication GB 2266176 940202 Other publication GB 2266176 940202 Other publication GB 2166179 940705                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ram,H.,<br>nd Lewis,I.                     | Other publication CN 1099801 950308 Other publication DE 43933817 950427 Other publication DE 43933817 950427 Other publication NO 950123 950315 Other publication ZA 9305126 950116 Other publication FI 950171 950313. FEATURES Location/Qualifiers 1. 945 organism="unidentified" /mol_type="unassigned DNA" /db xref="taxon:32644"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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PD 08-OCT-2002
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CDS (4), (393).
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1 (bases 1 to 408)

Hale,J.E., Hershberger,C.L., Larson,J.L. an Recombinant synthesis of beta-lipotropin an Recombinant synthesis of beta-lipotropin an Patent: JP 2002533072-A 6 08-OCT-2002;

ELI LILLY AND CO
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1 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

1 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

1 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

1 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

1 Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

1 Hale, J.E., Hershberger, J.L. and Menke, M.A.

1 Hale, J.E., Hershberger, J.L. and Menke, M.A.

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Hale, J. E., Hershberger, C.L., Larson, J.L. and Menke, M.A.
AUTHORS
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Hale, J. E., Hershberger, C.L., Larson, J.L. and Menke, M.A.
AUTHORS
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Hale, J. E., Hershberger, C.L., Larson, J.L. and Menke, M.A.
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Hale, J. E., Hershberger, C.L., Larson, J.L. and Menke, M.A.
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## SUMMARIES

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TITLE

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Days

| 4.4                                      |          | c 42              | 41                 | 40                 | 39       | 38               | 37       | 36               | ω<br>5           | 34       | မ        | 32       | 31       | 30       | 29       | 28       | 27       | 26       |          | C 24     |          |  |
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| 462<br>496                               | 461      | 460               | 459                | 458                | 451      | 451              | 447      | 442              | 439              | 435      | 431      | 413      | 411      | 398      | 397      | 393      | 323      | 315      | 766      | 705      | 591      |  |
| N Ø                                      | N        | _                 | œ                  | œ                  | œ        | œ                | œ        | œ                | œ                | N        | 8        | æ        | w        | æ        | μ        | Н        | N        | N        | μ        |          | 7        |  |
| DN347146<br>BE663231                     | BG691533 | AV593657          | DN347234           | DN347142           | DN347334 | DN346863         | DN347081 | DN346969         | DN347054         | BF230607 | DN349208 | DN348158 | BI542423 | DN347669 | AW484007 | AW658405 | BE482262 | BE482263 | AA843141 | AI031553 | CK951411 |  |
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# RESULT 1 T29548 LOCUS DEFINITION T29548 339 bp mRNA linear EST 06-SEP-1995 EST83988 Human Parathyroid gland Homo sapiens cDNA 5' end similar to parathyroid hormone (HT:2194), mRNA sequence. T29548.1 GI:611646

ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM Hominidae; Homo.

1 (bases 1 to 339) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human)

JOURNAL PUBMED COMMENT RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkledr, P.S., Kelley, J.C., Liu, L.-I., Marmarous, S.M., Merrick, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmarous, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bedmarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Gruber, J., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Yu, G., Liu, L., Li, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G., Liu, L., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G., L., Charlettie, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence

AL Nature 377, 3-174 (1995)

ED 7566098

Contact: Venter, J.C.

The Institute for Genomic Research 1982 Sequence 1983 Sequence 20878

Fax: 3018699056

Fax: 3018699056

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JOURNAL
PUBMED
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KEYWORDS
SOURCE
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AA372113
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DEFINITION
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AUTHORS
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source
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1 (bases 1 to 316)

2 (bases 1 to 316)

Rodams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S., Fitzgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Philips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E. J., Dinke, D., Peng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P. J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

Other ESTs: THC179155

Contact: Kerlavage, AR

Bioinformarics
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   Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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AA372113 AA372113
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   Seq
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Contact: Wilson RK
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
   W19763
324 bp mRNA linear EST 03-MAY-1996
zb39c01.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:305952 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
  Hominidae; Homo.

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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Alikin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Waterston, R., Williamson, A., Wohldmann, P. and Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.
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n,G., Marra,M.,
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   Not I;
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JOURNAL
  Query Match
Best Local (
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  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
   Unpublished (1995)
Contact: Wilson RK
   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   Mammalia; Eutheria;
   Eukaryota; Metazoa;
  Similarity
   IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
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   UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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  CUGUTUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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  314 286 1800
314 286 1810
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  Score 38.8; DB Pred. No. 0.29; 4; Mismatches
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   Length 324;
  š
  63108
   EST 15-MAY-1996
  Not I;
   , н
Н н -
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Fax: 314 286 1810
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  Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  ното вартепв
   (HUMAN);, mRNA sequence. W38966
   zb28b12.rl Soares parathyroid rumor NbHPA Homo sapiens cDNA clone IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
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  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
  The WashU-Merck EST Project
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Unpublished (1995)
Conteact wilson RK
Conteact Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
  Hominidae; Homo.

1 (bases 1 to 411)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soarces, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soarces, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Pred. No. 0.45;
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   8
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   Length
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   63108
  Marra, M.,
   ٥,
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  231
   61
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Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NTH."
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밁 Ś 망 Ś

TITLE
JOURNAL
PUBMED
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810 Contact: Wilson RK <u>3</u> 63108

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  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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  Tel: 314 286 1800
Fax: 314 286 1810
   Unpublished (1995)
Contact: Wilson RK
   Eukaryota;
   The WashU-Merck EST Project
   Hominidae; Homo
   Mammalia; Eutheria;
   W38764.1 GI:1320471
   (HUMAN);, mRNA sequence.
  Similarity
   TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 124
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
  CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
   (bases 1 to 434)
  primer: mob.REGA+ET
  quality sequence stop: 253.
Location/Qualifiers
  Conservative
  cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
  TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3
  mol_type="mRNA"
db_xref="GDB:1248198"
  organism="Homo sapiens"
   Metazoa;
  xref="taxon:9606"
  41.1%;
  14;
   Euarchontoglires; Primates;
   Chordata; Craniata; Vertebrata; Euteleostomi;
  Score 38.2; DB Pred. No. 0.46; 4; Mismatches
   434 bp
   mRNA
  DB 8;
  33
•
  Louis, MO
  Length
  Indels
   linear
   Catarrhini;
  416;
  63108
   Marra, M.,
   EST 15-MAY-1996
  0
```

8 á 밁 Ś

> 문 S 문 Ś

```
RESULT
W56235
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   SOURCE
   KEYWORDS
  VERSION
  ACCESSION
  DEFINITION
   ORIGIN
   Matches
   Query Match
   JOURNAL
   AUTHORS
   ORGANISM
   Best
  9
   Local Similarity
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
   Ŋ
   44;
  Unpublished (1995)
Contact: Wilson RK
  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Homo sapiens
  EST
   zc01e11.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:321068 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
  W56235
   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 865 Std Error: 0.00
  Tel: 314 286 1800
Fax: 314 286 1810
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
   The WashU-Merck EST Project
  W56235.1 GI:1358124
  W56235
   Seq primer: mob.REGA+ET
  Email: est@watson.wustl.edu
   Wilson, R.
   Hominidae; Homo.
   (HUMAN);, mRNA sequence.
  TAGAATGGCTGCGTAAGAAGCTGCAGGATGT
  CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG
   (bases 1 to 450)
   sapiens (human)
   Conservative
   normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
  /tissue type="parathyroid tumor"
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/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Torgan: parathyroid_gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3
  db_xref="GDB:1258726"
   Tom/
   organism="Homo sapiens"
   ocation/Qualifiers
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   db_xref="taxon:9606"
   41.1%;
48.4%;
   _type="mRNA"
   14; Mismatches
   Score
Pred.
  450 bp
   38.2;
No. 0.
   DB
.46;
  mRNA
   8
   Length 434;
  linear
   MO 63108
  EST 10-OCT-1996
   0
   Gaps
   233
   61
   0
```

vector (Pharmacia). Library went through one round

밁 Ś 밁 δ

RESULT W56820

밁 Ş 문 Ş ORIGIN

```
REFERENCE
AUTHORS
  ACCESSION
VERSION
KEYWORDS
  RESULT
W33077
   COMMENT
  SOURCE
ORGANISM
   FEATURES
   DEFINITION
  source
  249
  189
  62
  N
  The WashU-Merck EST Project
Unpublished (1995)
Contact: wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
   453 bp mRNA linear EST 10-OCT-1996 zc07al2.rl Soares parathyroid tumor NDHPA Homo sapiens cDNA clone IMAGE:321598 5' similar to gb. V00597 PARATHYROID HORMONE PRECURSOR W33077
  44;
  Hominidae; Homo.

1 (bases 1 to 453)

1 (bases 1 to 453)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  W33077
W33077.1 GI:1315062
  Insert Length: 871 State
Seq primer: mob.REGA+ET
  Similarity
  : |||:||:||:|| || |:||||| |:
TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
  ĊŢĠŢĠĄĠŢĠĄĄĄŢĄĊĄĠĊŢŢĄŢĠĊĄŢĄĄCĊŢĠĠĄĄĄĄCĄŢĊŢĠĄĄCŢĊĠĄŢĠĠĄĠĄĠĄĠ
   cuguruncceaaaauccaeauecuecuecuecuecuecuecuecuecuecuecauccauecaa
  quality sequence stop: 367.
Location/Qualifiers
  314 286 1800
314 286 1810
  Conservative
  normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
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/tissue_type="parathyroid tumor"
/tissue_type="parathyroid tumor"
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/clone_lib="Soares_parathyroid tumor_NbHPA"
/clone_lib="Soares_parathyroid gland; VecTor: pT7T3D
/note="Organ: parathyroid gland; VecTor: pT7T3D
(pharmacia) with a modified polylinker; Site_1:
Site_2: Eco Ri; ist strand cDNA was primed with
  9,6
   1. .453
  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1259256"
/db_xref="taxon:9606"
  41.18; 48.48;
  Score 38.2;
Pred. No. 0.
  Mismatches
   DB
.46;
  Length 450;
  ٥,
  Not I;
a Not I -
  Gaps
  248
  61
```

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   REFERENCE
AUTHORS
   FEATURES
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   TITLE
JOURNAL
   Matches
  Query Match
Best Local
  261
  201
  62
  Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
   N
  W56820

writer was a second was a second was selected with the way of the way
  1 (bases 1 to 496)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Holman,M., Hultman,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  EST
  The WashU-Merck EST Project
  W56820.1 GI:1358743
   W56820
  Hominidae; Homo.
   Homo sapiens (human)
  Similarity
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
  CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG
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   / Organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo sapiens"
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//db_xref="GDB:1258064"
//clone="IMAGE:321004"
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//dev_stage="adult"
//dev_stage="ad
   quality sequence stop: 424.
Location/Qualifiers
   Conservative
   normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatina Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
TTTTT-3'], double-stranded cDNA was size selected, li
to Eco RI adapters (Pharmacia), digested with Not I a
cloned into the Not I and Eco RI sites of a modified
vector (Pharmacia). Library went through one round of
  mRNA sequence.
   14;
   Score 38.2; DE Pred. No. 0.46; Mismatches
  92
  DB,
   33;
   8
   Louis,
   Length
   Indels
   ð
   0
  260
```

COMMENT

ORIGIN

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REFERENCE
AUTHORS
   RESULT
W19765
  १
   밁
   Ś
  COMMENT
   밁
   ORIGIN
   FEATURES
  SOURCE
  KEYWORDS
  VERSION
  ACCESSION
   DEFINITION
   Matches
  TITLE
  ORGANISM
  JOURNAL
   source
  Local Similarity
  179
   239
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92 : |||:|||:|||:|| || |:|||||| |:
   44;
   N
   w19765 536 bp mRNA linear EST 03-W
zb39c03.r1 Soares parathyroid tumor NbHPA Homo sapiens CDNA
IMAGE 305956 5' sīmilar to gb:V00597 PARATHYROID HORMONE PRE
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Lie, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homo sapiens
   W19765.1 GI:1295882
  Contact: Wilson RK
  Unpublished (1995)
  The WashU-Merck EST Project
   Hominidae; Homo
   lomo sapiens (human)
   (HUMAN);, mRNA sequence.
  cuguruccgaaauccagcugaugcacgugguggugguggugguuccauggaacgug 61
   TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 269
  CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTĆGATGGAGAGAG
  (bases 1 to 536)
  314 286 1800
314 286 1810
  quality sequence stop: 352.
   Conservative
  normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento
  /clone="IMAGE:305956"
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Site 2: Eco RI; lst strand cDNA was primed with a Not I -
   to Eco RI adapters (Pharmacia),
  /mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
  ocation/Qualifiers
   organism="Homo sapiens"
   41.18;
   14; Mismatches
   double-stranded cDNA was size selected, ligatedapters (Pharmacia), digested with Not I and
   Score 38.2; DB Pred. No. 0.47;
  В
   33;
   8
  Length
  Indels
   496
  contact the
   EST 03-MAY-1996
   0
   PRECURSOR
  Gaps
  ligated
   238
  0
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TITLE
JOURNAL
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AUTHORS
   VERSION
KEYWORDS
   FEATURES
   ACCESSION
   DEFINITION
   Matches
   Query Match
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  249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
   44;
   Unpublished (1995)
Contact: Wilson RK
  1 (bases 1 to 576)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   W56120.1 GI:1358009
EST.
  zc56h06.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   W56120
   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length; 904 Std Error: 0.00
   Tel: 314 286 1800
Fax: 314 286 1810
   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
  The WashU-Merck EST Project
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Homo sapiens
   Seq primer: mob.REGA+ET
  Wilson, R
  Hominidae; Homo.
   Email: est@watson.wustl.edu
   łomo sapiens (human)
  (HUMAN);, mRNA sequence.
   CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 248
  quality sequence stop: 433.
Location/Qualifiers
   Conservative
  Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
TTTTT-3/], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento
  /clone lib="Soares parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
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Site_2: Eco RI; 1st strand cDNA was primed with
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   organism="Homo sapiens"
  db_xref="taxon:9606"
  . .576
  41.1%;
   14;
   Score 38.2; DB Pred. No. 0.47;
  Mismatches
  Box 8501, St. Louis,
   ďď
  92
   mRNA
  33;
   8
   Length 536;
   Indels
   linear
  3
   Marra,M.,
  EST 11-OCT-1996
  0;
   Not I;
a Not I -
  Gaps
  61
  0
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RESULT W56120

FOCUS

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```
REFERENCE
AUTHORS
  SOURCE
ORGANISM
   ACCESSION
VERSION
KEYWORDS
  DEFINITION
   Local
  184 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGA 243
   244
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
: |||:|||:|||:|| || |:|||||| |:
244 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 274
   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
   44;
   The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4791: 314 286 1800
   1 (bases 1 to 583)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsonskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
  W39202

S83 bp mRNA linear EST 15-MAY-1996
zb35h03.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone
zh36521 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
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  (HUMAN);, mRNA sequence.
   Similarity
   314 286 1800
314 286 1810
   quality sequence stop:
Location/Qualifiers
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/lab_host="DH:10B (ampicillin resistant)"
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/note="Organ: parathyroid gland; Vector: pTT3T
/note="Organ: pTT3"
/note="Organ: parathyroid gland; Vector: pTT3T
/note="Organ: pTT3"
/note="Organ: 
   Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
  41.1%; Score 38.2; DB 8; 48.4%; Pred. No. 0.47;
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  400.
  33;
   Length 576;
   Indels
  0
  Gaps
  TITLE
JOURNAL
COMMENT
  REFERENCE
AUTHORS
   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   RESULT 15
BH958789/c
LOCUS
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   В
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  밁
   Ś
   ğ
   δ
  ORIGIN
  FEATURES
   ORIGIN
  DEFINITION
   Query Match
Best Local S
Matches 37
   Query Match
Best Local S
Matches 44
   source
   999
  67
  7
   1 Similarity 37; Conserv
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FEATURES

Conservative

41.1%;

; Score 38.2; I; Pred. No. 0.49

DB ,.49;

9;

Length 702; Indels

23;

0

Gaps

0

GACATTGATACAAGA 592 UGGCUGCGUAAAAAA 81 COMMENT

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113
  62
   53
   sequence.
BH958789
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Brassica oleracea
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Brassicaceae; Brassica.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 702)
1 (bases I to 702)
1 (bases I to 702)
2 (bases I to 702)
3 (bases I to 702)
4 (bases I to 702)
4 (bases I to 702)
5 (bases I to 702)
6 (bases I to 702)
6 (bases I to 702)
7 (bases I to 702)
8 (bases 
  Plate: odj08 row: c column
Seg primer: -21UPpOT forward
Class: shotgun
   SSD
   BH958789.1
  BH958789 702 bp DNA linear odj08c01.bl B.oleracea002 Brassica oleracea genomic,
  Similarity
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
  TAGAATGGCTGCGTAAGAAGCTGCAGGATGT
   CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG
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  quality sequence start: 17 quality sequence stop: 551. Location/Qualifiers
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/clone lib="B.oleracea002"
/note="Vector: pOTM13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
   adenomas was kindly provided by Dr. Institute of Diabetes and Digestive NIH."
  GI:23440016
   41.1%; Score
48.4%; Pred.
   Mismatches
   38.2; DB
No. 0.48;
   92
   33;
  8
  Length 583;
  Stephen Marx, National and Kidney Diseases,
   GSS 01-OCT-2002
   0
   Gaps
  112
  61
  0
```

RESULT W39202 LOCUS

밁 Ş В Ş

Matches

Search completed: November 24, 2005, 01:30:29 Job time: 1824 secs

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Result
No.
  Minimum DB seq
Maximum DB seq
   Database
  Total number of hits satisfying chosen parameters:
  Searched:
   Scoring table:
   Sequence:
   Perfect score:
   Title:
   OM nucleic -
  Post-processing:
   იიი
   on:
   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
   Score
41.4
38.2
   nucleic search, using
  Issued_Patents NA:*

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93
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Patent No. 5747453
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APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF INCREASING THE
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  Query Match
Best Local S
  NUMBER OF SEQUENCES:
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| Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli<br>Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 5,  |     |                  |                  |                  |                   |                     |                     |                    | 51,              |                     |                     | 6               | Sequence 5, A |              | ູຕ              | 31,       | 30,     | ,           | pequence 1, 5   |

ALIGNMENTS

#### GENERAL INFORMATION: APPLICANT: Jung, Bun-Kyung APPLICANT: Park, Doo-Hong APPLICANT: Chung, Soo II TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE FILE REFERENCE: 0136/06676 CURRENT APPLICATION NUMBER: US/09/463,282D CURRENT FILING DATE: 2000-01-20 PRIOR APPLICATION NUMBER: PCT/KR98/00146 PRIOR APPLICATION NUMBER: PCT/KR98/00146 PRIOR APPLICATION NUMBER: WE 1997-35230 PRIOR APPLICATION NUMBER: KE 1997-35230 PRIOR FILING DATE: 1997-07-27 NUMBER OF SEQ ID NOS: 26 Sequence 26, Application US/09463282D Patent No. 6500647 SOFTWARE: PatentIn version 3.1 Watch 61.1%; Score 56.8; DB 3; Local Similarity 54.3%; Pred. No. 3.3e-09; Pres 50; Conservative 20; Mismatches 22 62 TTGAATGGCTGCGTAAAAAACTGCAGGATGTT 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 2 CUGUTUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGAACGUG DB 3; Length 258; Indels 0; Gaps 61

POLYPEPTIDES

CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA: US/08/468,275
APPLICATION NUMBER: US/08/468,275
EILING DATE: 06-JUN-1995
CLASSIFICATION: 514
APPLICATION: 514
  TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
  ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
ZIF: 94303-0802

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
  TOPOLOGY: lir
MOLECULE TYPE:
FEATURE:
NAME/KEY: CDS
   APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
   LOCATION: FEATURE:
  CORRESPONDENCE ADDRESS:
   STREET: 950 PAGE MILL ROAD CITY: PALO ALTO STATE: CALIFORNIA
  LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
LECULE TYPE: DNA (genomic)
   NAME/KEY: mat_peptide
LOCATION: 25
  COUNTRY: USA
ZIP: 94303-0802
  STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
  COUNTRY:
  ADDRESSEE:
  86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   1 Similarity 56.0
51; Conservative
   CALIFORNIA
   USA
   CDS
7..138
  ALZA CORPORATION
   58.3%; Score 54.2; DB 2; 56.0%; Pred. No. 1.9e-08; tive 17; Mismatches 23;
  Release #1.0, Version #1.30
  O360-0002; ARC-2349
  Length 141;
   Indels
   0;
   Gaps
   0
  Ś
  밁
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   Matches
                                   TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
  TELEPHONE:
```

```
ATIORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION UNMER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (415) 496-8048
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STEANDENNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
US-08-468-275-5
   RESULT 4
US-09-007-466-3
  ; Sequence 3, Applicatio:
patent No. 6313092
GENERAL INFORMATION:
APPLICANT: HOLLADA
APPLICANT: OLDENBU
   Query Match
Best Local :
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UDATA:
PRIOR APPLICATION UNMER: US 08/468,275
PILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION UNUBER: 30,661
REFERENCE/DOCKET UNUBER: 0360-0002;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
   COUNTRY: USA
ZIP: 94303-0802
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUURENT APPLICATION NUMBER: US/09/007,466
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
  CORRESPONDENCE ADDRESS
  NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
   ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
   / Match 58.3%; Score 54.2; DB 2;
Local Similarity 56.0%; Pred. No. 1.9e-08;
les 51; Conservative 17; Mismatches 23;
  FILING DATE:
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  56 TIGAATGGCTGCGTAAAAAACTGCAGGACGT 26
   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
  2 cueurucceaaauccaecueauecaceeueeueeueeueeueeueeuuccaueeaaceue
   Application US/09007466
  HOLLADAY, LESLIE A.
OLDERBURG, KEVIN R.
VENTION: METHOD FOR INCREASING THE
AVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
                               O360-0002; ARC-2349
   0360-0002; ARC-2349
  Length 141;
   Indels
  0;
   Gaps
   57
  61
   0
```

; 141 base pairs nucleic acid

(415) 496-8150

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   US-09-007-466-5/c
   RESULT 5
   US-09-007-466-3
  Sequence 5, Application US/09007466 Patent No. 6313092
  Matches
   Query Match
Query Match
Best Local Similarity 56.0
Matches 51; Conservative
  GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
   TELEFAX: (415) 496-8048 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
  CURRENT APPLICATION NUMBER: US/09/no7
  FEATURE:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
  REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
  FEATURE:
  MOLECULE TYPE:
  STREET: 550 ALTO CITY: PALO ALTO
   CORRESPONDENCE ADDRESS:
  NAME/KEY:
LOCATION:
  NAME/KEY:
LOCATION:
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   TOPOLOGY: 11
   TYPE: nucleic acid
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   950 PAGE MILL ROAD
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   linear
   ALZA CORPORATION
  DNA (genomic)
   single
   58.3%; Score 54.2; DB 3; 56.0%; Pred. No. 1.9e-08; 56.0%; Mismatches 23;
  METHOD FOR INCREASING THE ELECTROTRANSPORT FLUX OF POLYPEPTIDES
 58.3%; Score 54.2; DB 3;
56.0%; Pred. No. 1.9e-08;
tive 17; Mismatches 23
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   O360-0002; ARC-2349
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    Gaps
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; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-952-980B-3
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   US-08-952-980B-3
  RESULT 6
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   Sequence 3, Application US/08952980B Patent No. 6333189
  Query Match 58.3%; Score 54.2; DB 3; Best Local Similarity 56.0%; Pred. No. 1.9e-08; Matches 51; Conservative 17; Mismatches 23;
  TELEFAX: (650) 496-80 INFORMATION FOR SEQ ID NO:
   GENERAL INFORMATION:
   REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
   ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,
  COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIFICATION: 530
CLASSIFICATION: 530
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
  APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
  SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
  NUMBER OF SEQUENCES:
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   MOLECULE TYPE:
   CITY: PALO ALTO
   STREET:
   TOPOLOGY:
  COUNTRY:
  NAME/KEY:
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  TELEPHONE:
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                     62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUCCAUGGAACGUG
  94303-0802
  2 CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGGAACGUG 61
  TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26
  CALIFORNIA
   950 PAGE MILL ROAD
  (650) 496-8150
(650) 496-8048
  USA
   mat_peptide
25
  7..138
  Sg
   linear
  DNA (genomic)
   single
   30,661
  ω
••
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  CIP 1
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   Indels
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   57
  61
  85
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RESULT 7 US-08-952-980B-5/c

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5, Application US/08952980B

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US-08-142-551B-8
US-08-142-551B-8
Sequence 8, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING
   밁
   Ş
  밁
  Ş
  US-08-952-980B-5
   Query Match
Best Local S
Matches 51
   Patent No. 63377110N:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIETCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION UNMBER: 2349 CIP 1
REFERENCE/DOCKET NUMBER: 2349 CIP 1
TELECOMMUNICATION INFORMATION:
   TITLE OF INVENTION: METHOD FOR TITLE OF INVENTION: ELECTROTRAN NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION STREET: 950 PAGE MILL ROAD
  SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
  TELEFAX: (650) 496-8048 INFORMATION FOR SEQ ID NO: 5:
   NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  APPLICANT: HOLLADAY, LESLIE A. APPLICANT: OLDENBURG, KEVIN R.
   STREET: 950 PAGE MI
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
   TELEPHONE:
   56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   Ch 58.3%; Score 54.2; DB 3; Length 141; I Similarity 56.0%; Pred. No. 1.9e-08; 51; Conservative 17; Mismatches 23; Indels
   94303-0802
   (650) 496-8150
  DNA (genomic)
   METHOD FOR INCREASING ELECTROTRANSPORT FLUX
   US/08/952,980B
   2349 CIP 1
  Version
   THE OF POLYPEPTIDES
  #1.30
  SAME
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   Gaps
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OTHER INFORMATION: poptide of interest"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 175..207

OTHER INFORMATION: fonte= "Encodes amino acid sequence OTHER INFORMATION: having six histamines that serves as a tag for the OTHER INFORMATION: purification of the protein on a nickel column."

US-08-142-551B-8
  RESULT 9
US-08-733-446-58
   밁
  Ś
  밁
   Ś
                          Sequence 58, Application US/08733446
Patent No. 5856138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS.
TITLE OF INVENTION: FOODUCTION THEREOF
NUMBER OF SEQUENCES: 62
  TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
  Matches
   Query Match
Best Local
   PILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
  FILING DATE: 22-OCT-1992
ATTOREY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 0003
TBLECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
   LOCATION: 1..201 FEATURE:
  APPLICATION NUMBER:
  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/142,551B FILING DATE: 25-0CT-1993 CLASSIFICATION: 435
  FEATURE:
   FEATURE:
NAME/KEY:
CORRESPONDENCE ADDRESS
  NAME/KEY: misc feature LOCATION: 1..51
OTHER INFORMATION: /note OTHER INFORMATION: seque OTHER INFORMATION: inclu
   NAME/KEY: misc feature LOCATION: 70..174
   131 TTGAATGGCTGCGTAAAAACTGCAGGACGT 161
  71
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
  N
   Similarity
  CCGTTTCCGAAATCCAGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG
   сисииисседданисся системи се со   Conservative
   CDS
   58.3%; Score 54.2; DB 2; 56.0%; Pred. No. 2.2e-08; tive 17; Mismatches 23;
   /note= "Encodes the leader peptide
sequence that serves to direct the
inclusion bodies."
  US 08/077,296
   US 07/965,677
   US 07/898,219
   000324-010
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  23;
  Length 207;
  AND
  protein into
  Gaps
   130
  61
  0
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US-10-340-484-14
   RESULT 10
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  á
   US-08-733-446-58
   Sequence 14, Applicate Patent No. 6875739 GENERAL INFORMATION:
   Query Match 49.7%; Score 46.2; DB 2; Best Local Similarity 50.5%; Pred. No. 9.7e-06; Matches 46; Conservative 17; Mismatches 28;
  TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION NUMBER: US/10/340,484
CURRENT FILLING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR FILING DATE: 2002-01-10
   APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
  APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
   APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
   TELECOMMUNICATION INFORMATION: TELEPHONE: (617)523-3400
   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  TOPOLOGY: 11
   STREET: 130 m
  LOCATION:
   COMPUTER:
  COUNTRY:
   STATE:
  ADDRESSEE:
   LOCATION: 19...24
IDENTIFICATION METHOD:
   STRANDEDNESS: double
   NAME/KEY:
   ENGTH:
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   nucleic acid
   Massachusetts
  CTGTGTCCGAGATTCAGCTGCTGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG
  Application US/10340484
   130 Water Street
  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
  mutation
   SGS
  linear
  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
   1..252
  CUSHMAN
   Floppy disk
  other nucleic acid, synthetic DNA
   M
  Version #1.25
  Length 252;
   Indels
   0
   Gaps
  61
   0
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밁
   ; TYPE: DNA; ORGANISM: Homo sapiens US-10-340-484-14
  5
  밁
   á
  US-08-689-190-1
   RESULT 11
  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 102
   Sequence 1, Applic
Patent No. 5714349
   Matches
  Query Match
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/006,197
FILING DATE:
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
  PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
  TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 27
   APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
   TITLE OF INVENTION: SY.
TITLE OF INVENTION: PA.
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
   REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  APPLICANT:
 MOLECULE TYPE:
   APPLICANT:
   Local Similarity
   COUNTRY:
                     TOPOLOGY:
                                    STRANDEDNESS:
  ADDRESSEE:
  ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
   ENGTH:
   62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
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   45;
  Boston
  02109
  CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61
   cugurucceananuccaecueanecaceueeueeueeueeueeueeuuccaueeaaceue 61
  : 252 base pairs
   Application US/08689190
   Massachusetts
   130 Water Street
  YAMADA,
   OSHIKA,
   Conservative
  CUSHMAN
  Floppy disk
other nucleic acid, synthesizing DNA
                                      double
  Takao
   Tsunehiko
   SYNTHETIC GENE CODING FOR HUMAN PARATHYROID HORMONE
   48.0%; Score 44.6; DB 3;
49.5%; Pred. No. 2.5e-05;
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   Mismatches
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   Gaps
```

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RESULT 12
US-08-733-446-23
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   US-08-689-190-1
  CURRENT APPLICATION UNMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
APPLICATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPAX: (617)523-3640
TELEPAX: (617)523-3640
TELESTAX: 20029 STRE UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
   ; Sequence 23, Application; Patent No. 5856138; GENERAL INFORMATION: APPLICANT: FUKUDA,
  Query Match 48.0%;
Best Local Similarity 49.5%;
Matches 45; Conservative 1
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  FRATURE:
NAME/KEY: MUTATION
LOCATION: 7, 8, 9, 12, 15, 19, 21, 33, 36, 43, 51, 58,
IDENTIFICATION METHOD: S
   TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: PRODUCTION THEREOF NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
  MOLECULE TYPE:
   CITY: Boston
STATE: Massa
IDENTIFICATION METHOD:
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   STREET:
   ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
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  62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT
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  Massachusetts
   Application US/08733446
   130 Water Street
   CDS
1..252
   other nucleic acid,
Œ
   Ħ
  17;
  Score 44.6; DB 2;
Pred. No. 3.2e-05;
7; Mismatches 29;
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  92
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  Indels
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  Gaps
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  RESULT 13
US-08-733-446-56
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Query Match 48.0%; Score 44.6; DB 2; Best Local Similarity 49.5%; Pred. No. 3.2e-05; Matches 45; Conservative 17; Mismatches 29;
   TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
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SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
  Query Match 48.0%; Score 44.6; DB 2; Best Local Similarity 49.5%; Pred. No. 3.2e-05; Matches 45; Conservative 17; Mismatches 29
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GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER: U
   MOLECULE TYPE:
   CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
   TELEPHONE: (617)523-6440
   ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ADDRESSEE: CUSHMAN STREET: 130 Water Street
   NAME/KEY: mutation
LOCATION: 103...105
IDENTIFICATION METHOD:
  APPLICATION NUMBER: US/0 FILING DATE: 18-OCT-1996
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   6, Application US/08733446
5856138
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N: HUMAN PARATHYROID HORMONE MUTEINS AND
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  US/08/402,970
  US/08/733,446
  Version
   DB 2;
  29;
   ROBERTS
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US-08-835-231-34
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TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
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Query Match
Best Local Similarity
  PILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
  GENERAL INFORMATION:
APPLICANT: NISHIM
   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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PRIOR APPLICATION DATA:
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SOFTWARE: FastSEQ Version 1.5
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  APPLICANT: KOYAMA, No. 5861284UYUKi
APPLICANT: FUKUDA, TSunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
  FEATURE:
   FRAGMENT TYPE:
ORIGINAL SOURCE:
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HYPOTHETICAL: NO
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  NAME/KEY:
LOCATION:
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  STREET:
   REFERENCE/DOCKET NUMBER:
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  ORGANISM:
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  BOSTON
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  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  USA
   KURIYAMA,
  NISHIMURA, Osamu
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   41614-FWC
 Score 44.6; DB 2;
Pred. No. 3.2e-05;
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FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY_AGENT INFORMATION:
NAME: DAVID, RESNICK S
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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FILING DATE:
CLASSIFICATION: 435
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NAME/KEY:
   REFERENCE/DOCKET NUMBER: 41
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  NISHIMURA, Osamu
KURIYAMA, Masato
  617-523-6440
  USA
  Conservative
  KOYAMA, No. 6287806uyuki
  FUKUDA, Tsunehiko
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            Coding Sequence
  617-523-3400
  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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  METHOD FOR PRODUCING A BIOLOGICALLY ACTIVE RECOMBINANT CYSTEINE-FREE
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.
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93
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US-10-997-700-33
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60, Appl
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67,   APPLICANT: Wagner, F.
APPLICANT: Yia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
ITILE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2003-05-23
PRIOR PILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FRASTSEQ for Windows Version 4.0
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Sequence 60, Application US/10997078
Publication No. US20050221444A1
RESULT 2
US-10-997-700-33
; Sequence 33, Application US/10997700
; Publication No. US20050239172A1
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; OTHER INFORMATION:
US-10-997-078-60
  O
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   Publication No.
GENERAL INFORMATION:
Wagner, F.
   Query Match
Best Local
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47.6
47.6
47.6
44.6
44.2
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Maximum Minimum

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Scoring table: Sequence:

Title: Perfect score:

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Copyright

Result No.

Query Match

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Gaps

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   US-10-997-078-61
   밁
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   В
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   US-10-997-700-33
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Matches
   APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050221444A1
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  GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Peng, L.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
FILE REFERENCE: 1627,010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR PPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2003-05-23
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PRIOR FILING DATE: 2003-05-24
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19;

Indels

0,

Gaps

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; TYPE: DNA; ORGANISM: Artificial Sequence; FEATURE: ; FEATURE ; OTHER INFORMATION: A synthetic PTH sequence. US-10-997-078-141
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US-10-997-700-34
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US-10-997-700-34
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Publication No. US20056
FRENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Yeng, L.
APPLICANT: Xia, U.
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PRIOR FILING DATE: 2002-05-24
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   APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
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GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
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   APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627, 010US1
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CURRENT FILING DATE: 2004-11-24
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  z cugurucceaaauccaecueauecaceueeueeueeueeueeueeuuccaueeaaceue
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  Holmquist, B.
  Application US/10997700
No. US20050239172A1
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19; Mismatches
DB 9; L...
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APPLICANT: Wagner, F.
APPLICANT: Yia, U.
APPLICANT: Yia, U.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Nolmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for TITLE OF INVENTION: Methods and DNA Constructs for CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
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Sequence 62, App
Publication No. 1
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US-10-997-700-35
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  APPLICANT: Wagner, F.
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APPLICANT: Yia, U.
APPLICANT: Holmquist, B.
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APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627,010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 148
NUMBER OF SEQ ID NOS: 148
   Sequence 35, Application US/10997700 Publication No. US20050239172A1
  Matches
   Query Match
Best Local Similarity
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 62
  GENERAL INFORMATION:
  GENERAL INFORMATION:
   ORGANISM: Unknown FEATURE:
  TYPE: DNA
  ENGTH:
  53; Conservative
  62
   62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
   62
  252
   N
  N
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61
   TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
   Application US/10997078
  US20050221444A1
                          PTH(1-84)
  64.5%; Score 60; DB 9;
57.6%; Pred. No. 8e-11;
htive 19; Mismatches
   DB 9;
   for High Yield Production of Polypept
  20; Indels
   Length 252,
  ,
,
  Gaps
  61
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```
PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR PILING DATE: 2004-11-24
PRIOR PILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 276
Type: Prince   밁
   Ś
  밁
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  RESULT 8
US-10-997-700-89
   밁
  S
  В
   RESULT 9
US-10-997-762-18
  US-10-997-700-89
   GENERAL INFORMATION:
APPLICANT: Seo, Jin Seog
APPLICANT: Seo, Jin Seog
APPLICANT: Seo, Jin Seog
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REFERENCE: 1627.026US1
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
   GENERAL INFORMATION:
   Sequence 89, Application US/10997700 Publication No. US20050239172A1
   Matches
  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 89
   APPLICANT: Wagner,
APPLICANT: Peng, L
APPLICANT: Xia, U.
APPLICANT: Holmqui
  Sequence 18, Ap
Publication No.
  Matches
  Query Match
  Query Match
   Best Local Similarity
   CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
  APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
CURRENT FILING DATE: 2004-11-24
   LENGTH: 264
TYPE: DNA
ORGANISM: Artificial Sequence
  OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84)
  FEATURE:
  Local Similarity
mes 53; Conserv
  65
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   62
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU ::|||:|||:||:::
   N
  ហ
  53; Conservative
  Peng, L
Xia, U.
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
   ĊŢĠŢŢŢĊŢĠĀĀĀŢĊĊĀĠĊŢĠĀŢĠĊĀĊĀĀCCŢĠĠŢĀĀĀCACCŢĠĀĀCŢĠŢĀŢĠĠĀĀĊĠŢĠ
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  Application US/10997762
  Conservative
   F
  64.5%;
57.6%;
   64.5%;
57.6%;
  19;
   19;
   Score 60; DB 9;
Pred. No. 8e-11;
9; Mismatches
   Score 60; DB 9; Pred. No. 8.1e-11;
   Mismatches
   93
  96
   93
   20;
   Length 264;
  Length 252,
   Indels
   Indels
   0
   0
   Gaps
  Gaps
   64
  61
  61
  0
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```
Sequence 3, Application US/10997822
Publication No. US20050227314A1
GENERAL INFORMATION:
APPLICANT: Holmquist, B.
APPLICANT: Strydom, D.
APPLICANT: Genealk, X.
APPLICANT: Cryer, R.
TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
FILE REFERENCE: 1627.011US1
CURRENT APPLICATION UNMBER: US/10/997,822
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16647
PRIOR PILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,484
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 276
TYPE: DNA
ORGANISM: Artificial Sequence
Sequence 75, Application US/10997700
Publication No. US20050239172A1
GENERAL IMPORMATION:
APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Yis, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627.009US1
FILE REFERENCE: 1627.009US1
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
  US-10-997-700-75
   В
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   ş
  ; OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric US-10-997-822-3
   RESULT 10
US-10-997-822-3
   Ś
  밁
  δ
  ; OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic US-10-997-762-18
   Matches
  Query Match
Best Local
   Matches
   Query Match
Best Local (
  ORGANISM: Artificial Sequence FEATURE:
   FEATURE:
   173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264
  173
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   l Similarity 57.6
53; Conservative
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGGAACGUG
   53;
   Similarity
  TTGAATGGCTGCGTAAAAACTGCAGGACGTT 264
   Conservative
   64.5%; Score 60; DB 9; Length 276
57.6%; Pred. No. 8.2e-11;
  64.5%; Score 60; D
57.6%; Pred. No. 8.
   19;
   19;
   Mismatches
   Mismatches
  DB 9; Length 276
8.2e-11;
   20;
   20;
  for High Yield Production of Polypept
   Indels
   Indels
   0;
  protein
   protein
   Gaps
   Gaps
   232
   61
  61
   0
  RESULT 13
US-10-997-700-76
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  Query Match
Best Local S
Matches 53
  Query Match
Best Local S
Matches 53
       APPLICANT: Wagner,
APPLICANT: Peng, L
APPLICANT: Xia, U.
APPLICANT: Holmqui
  Sequence 76, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
  74
  62
                        Peng, L.
Xia, U.
```

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Sequence 133, Applicat,
Publication No. US2005;
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Yeng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist,
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; OTHER INFORMATION: A
US-10-997-700-75
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US-10-997-078-133
  US-10-997-078-133
   APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 133
LENGTH: 282
TYPE: DNA
ORGANISM: Artificial Sequence
  NUMBER OF SEQ ID NOS: 93
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 75
LENGTH: 276
TYPE: DNA
ORGANISM: Artificial Sequence
EPATTER
227 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 258
   167 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAACACCTGAACTCTATGGAACGTG
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  53;
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
  53;
   Similarity
  Similarity
  TIGAATGGCTGCGTAAAAAACTGCAGGACGTT 105
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  Application US/10997078 o. US20050221444A1
  Conservative
   Conservative
   Ή
.
   synthetic
   synthetic sequence
   64.5%;
57.6%;
   64.5%; Score 60; DB 9; L
57.6%; Pred. No. 8.2e-11;
tive 19; Mismatches 20;
  19;
  Score 60; DB 9;
Pred. No. 8.2e-11
9; Mismatches 2
  PCR
  product
   for the T7tagVg-PTH(1-34)
  .2e-11;
  20;
   Length 276;
  Length 282
  Indels
  Indels
  0
  0
  Gaps
  Gaps
   cassette.
  226
   61
   73
  13
```

**T**J

```
APPLICANT: Wagner, F.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for TITLE OF INVENTION: Methods and DNA Constructs for CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
  FILE REFERENCE: 1627-009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 291
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   RESULT 14
US-10-997-700-77
  ; OTHER INFORMATION: A synthetic US-10-997-700-76
   US-10-997-700-91
   RESULT 15
  US-10-997-700-77
  Query Match
Best Local Similarity
Matches 53; Conserv
Sequence 91, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
  Sequence 77, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
  Matches
  Query Match
Best Local (
   TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: DNA
   ORGANISM: Artificial FEATURE:
  OTHER INFORMATION: A synthetic PCR product.
  TYPE: DNA
   89
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   68
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   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
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TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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   PCR product.
   DB 9; Length 291
  for High Yield
  Indels
   0
  Production of Polypept
  Gaps
   Gaps
  88
   61
  0
   0;
```

APPLICANT: Wagner, F.

```
APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: ADDRICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic PILE REPERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR PILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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   Matches
   Query Match
Best Local Similarity
122 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
                                     62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  62 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   53;
   Conservative
   64.5%;
   19; Mismatches
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Pred. No. 8.5e-11;
Mismatches 20;
  DB 9; Length 321;
   Indels
   0,
   Gaps
  121
   0
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Search completed: November 24, 2005, 04:46:56 Job time: 413.667 secs

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Title:
Perfect score:
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
  OM nucleic - nucleic search, using sw model
   Total number of hits satisfying chosen parameters:
   Searched:
   Scoring table:
  Sequence:
Published_Applications_NA_New:*

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8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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            1987654321
  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
   US-09-475-158A-15
93
  November 24, 2005, 01:30:39 ; Search time 195 Seconds (without alignments) 70.875 Million cell updates/sec
  3205263 seqs, 74304013 residues
  1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93
  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
   6410526
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 21<br>22<br>23                                              | c 19          | c 17          | 0 C C C C C C C C C C C C C C C C C C C |                                                              |                |                                        |      |                                        | ດ<br>ហ ≄ | с<br>. З    | c 1                                    | Result<br>No.    |
|-------------------------------------------------------------|---------------|---------------|-----------------------------------------|--------------------------------------------------------------|----------------|----------------------------------------|------|----------------------------------------|----------|-------------|----------------------------------------|------------------|
| 2 2 2 2<br>2 2 2 2                                          |               | 22.6          |                                         | ) N N<br>) N N<br>n on o                                     |                | 23<br>23                               | 23   | ω ω<br>•                               | ω.       | 24.2        | 28.4                                   | Score            |
|                                                             |               | 24.3          |                                         |                                                              |                |                                        |      |                                        |          |             | 30.5                                   | Query<br>Match 1 |
| 409<br>1254<br>1899                                         | 1984<br>55763 | 7989<br>14770 | 7979                                    | 7979                                                         | 481            | 3704<br>26323                          | 3507 | 1657<br>3893                           | 947      | 3138        | 2327<br>6497                           | Length I         |
| 444                                                         | 1             | μμ.           | <b>,</b> ,                              |                                                              | ب د            | 7                                      | ۲    |                                        |          | ٠,          | 44                                     | DB               |
| US-10-839-799-28<br>US-10-858-730-35<br>US-10-689-742-77    | -10-502-893-1 | -10-509-      | -10-509-921<br>-10-509-921              | US-10-509-921-9<br>US-10-509-921-9                           | -10-667-295-44 | US-10-509-422-3<br>US-11-005-030-1     | -10  | US-10-821-234-318<br>US-10-821-234-255 | 1        | -10-392-234 | US-10-821-234-760<br>US-10-821-234-839 | ID               |
| Sequence 28, Appl<br>Sequence 35, Appl<br>Sequence 77, Appl | 1,<br>1,<br>A | e 8,<br>e 26  | 12,                                     | Sequence 11, Appli<br>Sequence 9, Appli<br>Sequence 10, Appl | 114            | Sequence 3, Appli<br>Sequence 1, Appli | ۲    | Sequence 318, App<br>Sequence 255, App | 11,      | 15,         | Sequence 760, App<br>Sequence 839, App | Description      |

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

| 0<br>45            | 44                 | C 43               | 42                | c 41              | 40              | c 39             |                   | c 37             |                   | c 35               | 34                                            | 33              | c 32             | 31              | c 30              |                  | c 28              |                  |                  |                  | C 24               |
|--------------------|--------------------|--------------------|-------------------|-------------------|-----------------|------------------|-------------------|------------------|-------------------|--------------------|-----------------------------------------------|-----------------|------------------|-----------------|-------------------|------------------|-------------------|------------------|------------------|------------------|--------------------|
| 21.2               | 21.2               | 21.2               | 21.2              | 21.2              | 21.4            | 21.4             | 21.4              | 21.4             | 21.4              | 21.4               | 21.6                                          | 21.6            | 21.8             | 21.8            | 22                | 22               | 22                | 22               | 22               | 22               | 22                 |
| 22.8               | 22.8               | 22.8               | 22.8              | 22.8              | 23.0            | 23.0             | 23.0              | 23.0             | 23.0              | 23.0               | 23.2                                          | 23.2            | 23.4             | 23.4            | 23.7              | 23.7             | 23.7              | 23.7             | 23.7             | 23.7             | 23.7               |
| 4035               | 3701               | 3328               | 1392              | 59                | 12732           | 12391            | 3371              | 3305             | 2743              | 2458               | 1714                                          | 809             | 5796             | 3160            | 3393              | 2850             | 2748              | 2745             | 2727             | 2631             | 2043               |
| ب                  | Н                  | ب                  | Н                 | 7                 | μ               | 7                | Н                 | 7                | ۲                 | _                  | <u>, , , , , , , , , , , , , , , , , , , </u> | σ               | L                | œ               | 9                 | 9                | _                 | 9                | 9                | 9                | r                  |
| US-10-793-626-3525 | US-10-793-626-3392 | US-10-793-626-3644 | US-10-793-626-349 | US-11-040-159-127 | US-10-802-796-1 | US-11-017-550-67 | US-10-131-826A-35 | US-11-017-550-68 | US-10-821-234-267 | US-10-131-826A-387 | US-10-131-826A-251                            | US-11-132-839-6 | US-10-821-234-62 | US-11-112-944-8 | US-11-077-550-138 | US-11-077-550-67 | US-10-821-234-662 | US-11-077-550-59 | US-11-077-550-63 | US-11-077-550-65 | US-10-467-962B-100 |
| Sequence           | Sequence           | Sequence           | Sequence          | Sequence          |                 | Sequence         |                   |                  | Sequence          | Sequence           | Sequence                                      | Sequence        | Sequence         | Sequence        | Sequence          | Sequence         | Sequence          | Sequence         | Sequence         | Sequence         | Sequence           |
| 3525, A            | 3392, A            | 3644, A            | 349, AD           | 127, App          | 1, Appi         | 6/, App          | 35, App           | 68, App1         | 267, Apj          | 387, App           | 251, Ap                                       | 6, Appi         | 62, App1         | 8, Appli        | 138, App          | 67, App.         | ;                 |                  | 63, App          | 65, App.         | ~                  |

### ALIGNMENTS

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US-10-821-234-839
, Sequence 839, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
, APPLICANT: Labat, Ivan
, APPLICANT: Labat, Ivan
, APPLICANT: Andarmani, Susan
, APPLICANT: Andarmani, Susan
, APPLICANT: Tang, Y. Tom
   Ś
  밁
  Ś
   ; LENGTH: 2327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-760
   RESULT 1
US-10-821-234-760/c
   RESULT 2
  APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATB: 2004-04-07
PRIOR APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATB: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATB: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 760
SEQ ID NO 760
  Sequence 760, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
  Matches
  Query Match
  APPLICANT: Labat, Ivan
APPLICANT: Stache-Cra
   MacCH 30.5%; Score 28.4; DB 1; Length 2327; Local Similarity 44.9%; Pred. No. 0.82; es 35; Conservative 12: Migmathia
  834 GAGGATCTGCTGCAGGTT 817
  894 CAGCTGCCCCCTGGGTGGTGGAGGCCGTGACGACCATGATGGTGGCATTGGT 835
  16 CAGCUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGU 75
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; APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypep)
   CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT EILING DATE: 2004-04-07
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PRIOR TLING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
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US-10-392-234A-15/c
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  В
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  ; TYPE: DNA; ORGANISM: Homo sapiens US-10-821-234-839
  US-10-392-234A-15
  APPLICANT: Blarmacia and Upjohn Corporation
APPLICANT: Buxser, Steven
APPLICANT: Bocker, Steven
APPLICANT: Docker, Steven
APPLICANT: Docker, Douglas
APPLICANT: Ataznhi Li
TITLE OF INVENTION: Method for Screening for acrab Transporter Family Inhibitors
FILE REFERENCE: 6206
CURRENT APPLICATION NUMBER: US/10/392,234A
CURRENT APPLICATION NUMBER: US/60/364,935
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
SEQ ID NO 15
LENGTH: 3138
TYPE- NN
318
  Sequence 15, Application US/10392234A Publication No. US20050255538A1 GENERAL INFORMATION:
   Query Match
Best Local (
  Matches
  Matches
  Query Match
  TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
   / Match 26.5%; Score 24.6; I
Local Similarity 41.3%; Pred. No. 18;
les 26; Conservative 13; Mismatches
  OF INVENTION: Antigenic Polypeptides
   3204 ATG 3206
  137 TGCACGGCGATGGCCGGCGGGGGCGATGGCCGGGTACTGGTTGACCGGCAGACTGAGGATC 78
  83 UGCAGGACG 91
   23 UGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAAC 82
   62 UUG 64
   77 GACAGGCCG
  ch 26.0%; Score 24.2; D 1 Similarity 50.7%; Pred. No. 21; 35; Conservative 6; Mismatches
   2 cugurucceaaauccaecueauecaceeueeueeueeueeueeueeueeuuccaueeaaceue 61
   69
  DB 1;
  DB 1; Length 6497;
  28;
   24;
  Length 3138;
  Indels
  Indels
  ٥,
  0
  Gaps
```

```
CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/927,641

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036

PRIOR APPLICATION NUMBER: PCT/NZ 01/00115

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: U.S. NO. 09/724,624

PRIOR APPLICATION NUMBER: U.S. NO. 09/598,401

PR
   FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 5690
   밁
  Ś
  US-10-927-641-116/c
Sequence 116, Application US/10927641
Publication No. US20050244968A1
GENERAL INFORMATION:
   멍
  В
  Ś
  ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-116
  Ś
  ; TYPE: DNA ; ORGANISM: Staphylococcus aureus US-10-485-517-4
   Query Match
Best Local S
Matches 27
   Matches
  Query Match
Best Local
  APPLICANT: Wood, Marion
APPLICANT: Visser, Elizabeth
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036c4
   APPLICANT:
  Match 25.6%; Score 23.8; Local Similarity 40.3%; Pred. No. 32;
  520 GETETTTCCGGCTCGCTTGGTACTTCTGGTGTCGCTGGCGTTGGTGGCACGATTGGAGGT 579
528 ATGGTGGTGGTGGTGGTGGTGGTGGTGGTGAA 488
   580
  61 GUUGAAU 67
  27;
  Similarity
   Rice, Stephen
Eagleton, Clare
Lasham, Annette
   Conservative
   25.2%;
[larity 51.2%;
Conservative
   Ranjan
   13; Mismatches
  Score 23.4; DI
Pred. No. 29;
9; Mismatches
   9;
   DB 1;
  DB 1;
   11;
   27;
  Length 947;
  Length 5690;
   Indels
   0,
   0
   Gaps
   60
   0
```

```
RESULT 8
US-10-509-422-1/c
US-10-509-42-1/c
US-10-509-42-1/c
US-10-509-42-1/c
US-10-509-42-1/c
US-10-509-42-1/c
US-10-509-42-1/c
US-10-509-42-1/c
US-10-509-
  밁
   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-318
  밁
  ; LENGTH: 3893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-255
  US-10-821-234-255/c
   RESULT
  FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 3165
   GENERAL INFORMATION:
  Sequence 318, Appublication No.
   Query Match 24.9%; Score 23.2; DB 1; Length 3893; Best Local Similarity 43.2%; Pred. No. 47; Matches 19; Conservative 12; Mismatches 13; Indels 0
   SOFTWARE: pt_SEQ_genes Version 1.0 SEQ ID NO 255
   GENERAL INFORMATION
  Sequence 255, A Publication No.
   Best Local Similarity
   Query Match
   APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
  FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
   APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis
   APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human BMP2 Inducible Kinases
  ENGTH: 1657
  1231 TTTCCGAAGTCCATCAGGGGGGGGCGCGGCGGCAGGGGCGCGGGGCACTGGGGCCCGCG 1287
  31; Conservative
   Andarmani, Susan
   Application US/10821234 o. US20050255114A1
   Application US/10821234
o. US20050255114A1
   25.2%;
   ; Score 23.4; Di
; Pred. No. 33;
5; Mismatches
  and Treatment of Preeclampsia
   DB 1; Length 1657;
   21;
   Indels
   0
   0
   Gaps
   0;
```

GENERAL INFORMATION

APPLICANT: Aerssens, Jeroen APPLICANT: Athanasiou, Mar

APPLICANT:

APPLICANT:

Athanasiou, Maria Brain, Carlos Cohen, Nadine Dain, Bradley Denton, R. Rex Judson, Richard S.

Reed, Carol R.

Sequence 1, Application US/11005030 Publication No. US20050255495A1

```
FILE REFERENCE: 004974.01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: PCT/EP03/080825
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/367,512
PRIOR TILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 1
   ; LENGTH: 3507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-509-422-1
  á
   뭉
RESULT 10
US-11-005-030-1/c
   US-10-509-422-3
   RESULT 9
US-10-509-422-3/c
  Sequence 3, Application US/10509422
Publication No. US20050244825A1
GENERAL INFORMATION:
APPLICANT: Liou, Simon
   SEQ ID NO 3
LENGTH: 3704
TYPE: DNA
ORGANISM: Homo sapiens
  Matches
   Query Match 24.7%; Score 23; DB Best Local Similarity 46.8%; Pred. No. 54; Matches 22; Conservative 10; Mismatches
   Query Match
  Best Local Similarity
  PRIOR APPLICATION NUMBER: PCT/EP03/080825
PRIOR FILING DATE: 2003-03-20
PRIOR PPLICATION NUMBER: US 66/367,512
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR FILING DATE: 2002-08-30
   FILE REFERENCE: 004974.01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
  SOFTWARE: FastSEQ for Windows Version 4.0
   NUMBER OF SEQ ID NOS:
  TITLE OF INVENTION: Human BMP2 Inducible Kinases
   1509 CTGCTGCATATAAGCATCTTGAAGTAGGTGGTGGTGGTGGTGGT 1463
   |:| : | | | | | |:
1609 CIGCTGCATATAAGCATCTTGAAGTAGGTGGTGGTGGTGGTGGT
   22; Conservative
   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGU 48
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGU
  24.7%; Score 23; DB 1; Length 3507; 46.8%; Pred. No. 53;
  10; Mismatches
  DB 1; Length 3704;
  15;
  Indels
   48
   0,
  0
   Gaps
   0
  0
```

```
; APPLICANT: MASCIA, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11596-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/10/667,295
; PRIOR APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 481
  B
  Ś
   B
   ş
  ; NAME/KEY: misc_feature
; LOCATION: (16546)..(16546)
; OTHER INFORMATION: n is 'g' or 'a'
US-11-005-030-1
  US-10-667-295-44/c
  TITLE OF INVENTION: SLC5A7 Genetic Markers Associated with Age of Onset of TITLE OF INVENTION: Alzheimer's Disease FILE REFERENCE: 2300.009001

CURRENT APPLICATION NUMBER: US/11/005,030

CURRENT FILING DATE: 2004-12-07

PRIOR APPLICATION UNUMBER: US 60/529,999

PRIOR FILING DATE: 2003-12-15

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.3

SEQ ID NO 1
  Sequence 44, Application US/10667295
Publication No. US20050257293A1
GENERAL INFORMATION:
   Matches
  Query Match
    TYPE: DNA
   LENGTH: 26323
TYPE: DNA
ORGANISM: Homo sapiens
  NAME/KEY: misc feature
LOCATION: (1973)..(1973)
OTHER INFORMATION: n is
  LOCATION: (16520)..(16520)
OTHER INFORMATION: n is 'c'
  LOCATION: (7671)..(7671)
OTHER INFORMATION: n is
   LOCATION: (2273)..(2273)
OTHER INFORMATION: n is 'a'
  LOCATION: (2010)..(2010)
OTHER INFORMATION: n is 't'
   NAME/KEY: misc_feature
LOCATION: (2010)..(201
  NAME/KEY: misc feature LOCATION: (2273)...(227
   NAME/KEY: misc_feature
  JOCATION: (7671)..(767
   AME/KEY: misc feature
   watch 24.7%; Cocal Similarity 47.9%; 34; Conservative
  23891 TAGGTGCAGCA 23881
   INFORMATION: n is 't'
   79 AAACUGCAGGA 89
  19 CUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAAA 78
  'g' or 'a'
   얹
  or 't'
   or 'g'
  or 't'
   or 'c'
   7; Mismatches
   Score 23; DB
Pred. No. 83;
   ύ
   DB 7; Length 26323;
  30;
   Indels
   0
  Gaps
   B
  밁
Query Match
Best Local Similarity
  Matches
```

```
CURRENT APPLICATION NUMBER: US/10/021,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 119
SEQ ID NO 119
LENGTH: 2218
; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-509-921-9
  RESULT 13
US-10-509-921-9/c
   RESULT 12
US-10-821-234-119/c
   ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(481)
; OTHER INFORMATION: Ceres Seq. ID no. 6425497
US-10-667-295-44
  US-10-821-234-119
   Sequence 9, Application US/10509921
publication No. US20050250093A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicans
FILE REFERENCE: P51335
CURRENT APPLICATION NUMBER: US/10/509,921
CURRENT FILING DATE: 2004-10-01
   Sequence 119, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9
   Query Match
   Query Match
   PRIOR APPLICATION NUMBER: 60/369,685
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 54
   APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
   APPLICANT: Labat, APPLICANT: Stack
  TYPE: DNA
ORGANISM: Artificial Sequence
  ORGANISM: Homo sapiens
  TYPE: DNA
  ORGANISM: Brassica napus
  LENGTH: 7979
  / Match 24.3%;
Local Similarity 51.4%;
les 19; Conservative
   Local
  1753 GGTGGTGGTGGTGGTTGAGACAGGGTCTCTGTTG 1717
  399 CACTGGGTTCTCTTGAGTTGTTGTTTCATGGAAAATCTTAAGTGGCTGCCTAA 347
   28 GGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUG 64
   25 CACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAA 77
  h 24.3%; Score 22.6; DB 1;
Similarity 41.5%; Pred. No. 46;
22; Conservative 12; Mismatches 19;
  Ivan
                       The polynucle otide sequence encodes sequences from HCV {\it J4}\,({\it B/RI}) Replicons
  9; Mismatches
  Score 22.6;
Pred. No. 65;
  DB 1; Length 2218;
  19;
  9
  Length 481;
   Indels
  0
  0
  0,
  0
```

24.3%;

Score 22.6; Pred. No. 86;

DB 1;

```
Sequence 11, Application US/10509921

Publication No. US20050250093A1

GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation

TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons

FILTE REFERENCE: P51335

FURRENT APPLICATION NUMBER: US/10/509,921

CURRENT FILING DATE: 2004-10-01

PRIOR APPLICATION NUMBER: 60/369,685

PRIOR APPLICATION NUMBER: 60/369,685

PRIOR FILING DATE: 2002-04-03

NUMBER OF SEQ ID NOS: 54

SOFTMARE: PastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 7979

TYPE: DNA

ORGANISM: Artificial Sequence
   US-10-59-921-10/c
US-10-599-921-10/c
Sequence 10, Application US/10509921
Sequence 10, Application US/10509921
Publication No. US20050250093A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
FILE REFERENCE: P51335
FULE REFERENCE: P51335
CURRENT APPLICATION NUMBER: US/10/509,921
CURRENT FILING DATE: 2004-10-01
CURRENT FILING DATE: 2004-10-01
   RESULT 15
US-10-509-921-11/c
  Ś
   밁
   밁
  δ
  밁
   밁
  Ś
  ; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from ; OTHER INFORMATION: HCV J4(J4B/R1(C))Replicons US-10-509-921-10
  FEATURE:
OTHER INFORMATION: Thepolynucleotide sequence encodes
OTHER INFORMATION: HCV J4 Replicons
US-10-509-921-11
  RESULT 14
  SEQ ID NO 10
LENGTH: 7979
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
   Matches
   Query Match 24.3%; Score 22.6; D
Best Local Similarity 43.5%; Pred. No. 86;
Matches 30; Conservative 10; Mismatches
Query Match 24.3%; Score 22.6; DB 1; Best Local Similarity 43.5%; Pred. No. 86; Matches 30; Conservative 10; Mismatches 29;
   CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: 60/369,685
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
  2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61 |:|: || ||:|: || ||:|: || ||:|: || ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|:
   5674 GCAATGGGC 5666
  5734 CTGTCAGGACAACCGTCCTCTTTCTCCGTGGAGGTGGTATTGGAGGAGCCTTGGTAGGTG 5675
   5674 GCAATGGGC 5666
  62 UUGAAUGGC 70
   62 UUGAAUGGC 70
   30; Conservative
  2 CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
   10; Mismatches 29; Indels
  DB 1;
  29;
    29;
  Length 7979;
  Length 7979;
  Indels
    Indels
  sequences
   0,
   0
    0
   Gaps
   Gaps
    Gaps
   0
  0
    0;
```

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```
Title:
Perfect score:
Sequence:
   Regult
No.
   OM nucleic - nucleic search, using sw model
   Minimum DB seq length: 0
Maximum DB seq length: 200000000
  Scoring table:
  Database
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Total number of hits satisfying chosen parameters:
  O
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  10
11
12
13
14
15
16
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
   Query
Match
   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
  November 23, 2005, 22:35:17 ; Search time 1177.67 Seconds (without alignments) 4488.911 Million cell updates/sec
   1 gcuguuuccgaaaucggugg.....guaaaaaacugcaggacguu 93
   US-09-475-158A-16
93
  5883141 seqs, 28421725653 residues
  GenEmbl: *
   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
  gb ba:
gbenv:
gbon:
gbon:
gbon:
gbopat:
gbopat
   Length DB
    93
93
258
258
141
141
141
1441
1441
1441
1441
408
408
408
411
411
  BD266834
BD266833
BD266833
AR269042
AR005133
AR005133
AR177779
AR177779
AR177779
AR177780
AR177780
AR1383
BD234383
BD234385
BD234385
BD234386
BD234386
BD234386
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   SUMMARIES
  11766282
BD266834 PTH funct
BD266833 PTH funct
BD266833 PTH funct
AR269042 Sequence
AR005132 Sequence
AR005133 Sequence
AR177779 Sequence
AR177779 Sequence
AR177779 Sequence
AR173780 Sequence
AR17383 Recombina
BD234383 Recombina
BD234385 Recombina
BD234386 Recombina
BD234386 Recombina
BD234386 Recombina
BD234387 Recombina
BD234387 Recombina
  Description
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|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|----------|----------|----------|----------|--|
| 45                 | 44                | 43                 | 42                | 41                 | 40                | 39                 | 38                | 37                 | 36                | <b>35</b>          | ω<br>4            | ω<br>ω             | 32                | 31                 | 90                | 29                 | 28                 | 27                | 26                | 25                 | 24                | 23                | 22       | 21       | 20       | 19       |  |
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## ALIGNMENTS

| Query Match                           | FEATURES SOUTCE                                                                                        |                                                                                                                                                                                                                                                                                    |     | VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT                                                                                                                                                                                                                                                                                                                                                                         | RESULT 1 BD266834 LOCUS DEFINITION                                                                                                                       |
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PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
Patent: JP 2002533115-A 1 08-OCT-2002;

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E 1 (bases 1 to 93)

FTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

novel tethered ligand-receptor molecules

L Patent: JP 2002533115-A 2 08-OCT-2002;

THE GENERAL HOSPITAL CORP

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1 (bases 1 to 945)

Bauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gram, H.
Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Lew
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Lewis, I.

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  ORIGIN
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   COMMENT
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  TITLE
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  JOURNAL
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1 (bases 1 to 405)

2 Hale, J.E., Hershberger, C.L., Larson, J.L. and Mer Recombinant synthesis of beta-lipotropin and other patent: JP 2002533072-A 4 08-OCT-2002;

2 LI LILLY AND CO

OS Artificial Sequence
PN JP 2002533072-A/4

PD 08-OCT-2002

PF 15-DEC-1999 UP 2000589671

PF 15-DEC-1999 US 60/113058

PI 30HN EDWARD HALE, CHARLES LEE HERSHBERGER, JE PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JE PI MICHAEL ANDREW MENKE
PC C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N / C12N5/10, C12N9/50, PC C12P21/02, C12N15/00, C12N1
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BD234385
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BD234386
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   KEYWORDS
   VERSION
  POCUS
  AUTHORS
TITLE
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  Best Local
  Query Match
   JOURNAL
   JOURNAL
   source
ENCE 1 (bases 1 to 408)

YORS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

Recombinant synthesis of beta-lipotropin and other peptides

WAL Patent: JP 2002533072-A 7 08-OCT-2002;

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PN JP 2002533072-A/7

PD 08-OCT-2002

PR 15-DEC-1999 JP 2000589671

PR 11-DEC-1999 JF 2000589671

PR 21-DEC-1998 US 60/113058

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PI MICHAEL ANDREW MENKE
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PC C12P21/02, C12N15/00.C12N15/00.C12N5/10.
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Recombinant synthesis of beta-lipotropin and other peptides
Patent: JP 2002533072-A 6 08-OCT-2002;
ELI LILLY AND CO
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PD 08-OCT-2002
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08-CCT-2002
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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93
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| ADM14377<br>ADM14377<br>ADG93180<br>ADJ65858<br>ADM14375<br>ADG93260<br>AAT34865<br>AAG93181<br>ADG93181<br>ADG5859<br>ADJ65859<br>ADJ65859<br>ADJ65913<br>ADF90345                                                                             | AAA51731<br>AAA51729<br>AAA51730<br>AAT73910<br>ADG48030<br>ADG48059<br>ADG68786<br>ADG93179<br>ADG93179 | SUMMARIES                  |
| Adulai377 Human par<br>Adulai377 Human par<br>Adg93180 Novel exp<br>Adj65558 PTH pepti<br>Adw13375 Human par<br>Adg93360 Novel exp<br>Aat34865 Plasmid p<br>Adg93181 Novel exp<br>Adj65585 PTH prote<br>Adj65913 Tandem po<br>Adf90345 Chimeric | 51731 P 51729 P 51730 P 731730 S 748030 S 948059 948059 993179                                           | Description                |

| Ld                                                                                                                                                | X D D R                                               | YY<br>Iq                      | PA<br>PA<br>PA<br>PA                                                                               | Y PR               | Y P X                         | <b>1</b> 99     | Y PR               | **************************************                    | 80 0 X                                  | XXX                                                                     | X DE                                  | X D                | X A X              | RES<br>AAA<br>ID<br>XX                                   |            |                    |                    |                          |                    |                    |                    | a                  |                    |                    |                    |                                          |                    |                   |                    |                    |                            |                    |                    |
|---------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------|--------------------|-------------------------------|-----------------|--------------------|-----------------------------------------------------------|-----------------------------------------|-------------------------------------------------------------------------|---------------------------------------|--------------------|--------------------|----------------------------------------------------------|------------|--------------------|--------------------|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------------------------------|--------------------|-------------------|--------------------|--------------------|----------------------------|--------------------|--------------------|
| New<br>lind                                                                                                                                       | DR WPI; 2000-452384/39.<br>DR P-PSDB; AAY96974.<br>XX | PI Gardella TJ, Kronenberg    | PA (GARD/) GARDELLA T J. PA (KRON/) KRONENBERG H M PA (POTT/) POTTS J T. PA (JUEP/) JUEPPNER H. XX | 31-DEC-1998; 98US- | PF 30-DEC-1999; 99WO-US031108 | PD 06-JUL-2000. | PN WO200039278-A2. | Key<br>CDS                                                | OS Homo sapiens.<br>OS Synthetic.<br>XX | <pre>KW PTH; parathyroid hormone; KW resorption; remodeling; t XX</pre> | PTH functional                        | 31-OCT-2000 (first | AC AAA51731;<br>XX | RESULT 1<br>AAA51731<br>ID AAA51731 standard; RNA;<br>XX |            | 44 47.3            | 44 47.3            | 44 47.3                  | 44 47.3            | 44 47.3            | 44.6 48.0          | 37 44.6 48.0       | 36 45.2 48.6       | 46.2 49.7          | 46.2 49.7          | 49.4 53.1<br>46.4 49.9                   | 49.4 53.1          | 50.4 54.2         | 50.4 54.2          | 25 50.4 54.2 294   | 50.4 54.2                  | 50.4 54.2          | 50.4 54.2          |
| compound comprising an amino terminal signaling ted to a carboxy-terminal binding portion of parating mammalian conditions characterized by decre |                                                       | erg HM, Potts JT, Jueppner H; | î.                                                                                                 | 0114577₽.          | 3031108.                      |                 |                    | Location/Qualifiers<br>193<br>/*tag= a<br>/product= "PG9" |                                         | ne; conjugate; bone mass; bone; tether1; osteoporosis; ss.              | domain conjugate peptide PG9 coding s | entry)             |                    | , 93 BP.                                                 | ALIGNMENTS | 3 AAAS1456         | 3 AAA51459         | 3 AAA51454<br>3 AAA51453 | 3 AAA51455         | 3 AAĀ51452         | 2 AA055302         | 12 ADO42786        | 13 ADW80822        | 2 AAQ89923         | 2 AAQ89920         | 13 ADV69502<br>13 ADV69498               | 13 ADV69494        | 12 ADF90347       | 12 ADJ65917        | 2 AAT34866         | 12 ADJ65901<br>12 ADJ65900 | 12 ADG93252        | 12 ADJ65899        |
| aling functional domain f parathyroid hormone for decreases in bone mass.                                                                         |                                                       |                               |                                                                                                    |                    |                               |                 |                    |                                                           |                                         | reformation;                                                            | sequence.                             |                    |                    |                                                          |            | Maadiido Echo-Aien | Aaa51459 PCpB-APR- | Aaa51453 PCpB-ALY-       | Aaa51455 PCpB-LVPR | Aaa51452 PCpB-RVR- | Aaq55302 gp55-Asn- | Ado42/86 Human Fin | Adw80822 DNA encod | Aaq89923 Expressio | Aag89920 Recombina | Adv69502 Human par<br>Adv69498 Human par | Adv69494 Human par | Adf90347 Chimeric | Adj65917 Tandem po | Aat34866 Plasmid p | Adj65901 PTH DNA s         | Adg93252 Novel exp | Adj65899 PTH DNA s |

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  В
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  Query
Best L
  Matches
  Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing CAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inhalation unlike the large native PTH or PTH-rP which avoids the need for regular injections to treat osteoporosis
          New compound comprising an
   (GARD/)
(KRON/)
(POTT/)
   Claim 14; Fig 1; 119pp; English.
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   30-DEC-1999;
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) POTTS J T.
) JUEPPNER H.
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  99WO-US031108
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Homo sapiens. Synthetic.

Location/Qualifiers
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PTH; parathyroid hormone; conjugate; bone mass; bone resorption; remodeling; tether1; osteoporosis; ss.

domain conjugate peptide PG7

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31-OCT-2000

PTH functional

WPI; 2000-452384/39 P-PSDB; AAY96975.

Gardella TJ,

Kronenberg

Ĕ

Potts JT,

Jueppner

Η;

(GARD/) (KRON/) (POTT/)

) GARDELLA T J.
) KRONENBERG H M.
) POTTS J T.
) JUEPPNER H.

31-DEC-1998; 30-DEC-1999; 06-JUL-2000. WO200039278-A2

98US-0114577P 99WO-US031108

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RESULT 3
AAA5170
ID AAA5
XX AAA57
XX AAA5
XX PTH
XX
   밁
  δ
  В
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  Query Match
   Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) -R, are new, S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (wher n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is tipt. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cA in a mammalian cell having PTH-1 receptors or screening for a peptide non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
  linked to a carboxy-terminal binding portion of parathyroid treating mammalian conditions characterized by decreases in
   Sequence
   AAA51730 standard; RNA;
   61
  61
  H
   1
   81;
   Similarity
   GUUGAAUGGCUGCGUAAAAACUGCAGGACGUU
  GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
   GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGU
   93 BP; 21 A; 18 C; 30 G; 0 T;
   Conservative
   79.4%;
87.1%;
   93
   ВP
   0,
   Score 73.8; DB 3; Length 93; Pred. No. 2.5e-13; O; Mismatches 12; Indels
   24 U; 0 Other;
   93
  93
  hormone for bone mass.
   0,
   binding
R_1 is the
   Gaps
   need for
  s-(L)_n
   (where
  CAMP
  60
   60
   or
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1

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RRSULT 4
AA773010
ID AA777
XX AA777
XX AA777
XX AA777
XX Linh
DE Synt
XX Linh
XX Fec
XX Yec
X
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   밁
  밁
   ঠ
   Matches
   Query Match
Best Local &
  parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of BTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for
  Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of
   New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   Claim 14; Fig 1; 119pp; English.
  AAT73910
   AAT73910 standard; DNA; 152 BP.
  Sequence 93
  06-NOV-1996;
   WO9718314-A1
  misc_feature
   Homo sapiens.
  Synthetic
  recombinant
   Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein;
   Synthetic
   25-MAR-2003
  (BOEF )
   16-NOV-1995;
   5
   61
  -
   75;
   Similarity
  BOEHRINGER MANNHEIM GMBH
  injections to treat osteoporosis
   GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  GCUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGU
  еспецииссемму посеменнение поставление поставление в поставительной поставительного поставительног
   GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
   oligonucleotide encoding linker and PTH 1-37.
   production; endoproteinase LysC;
  BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;
   Conservative
  (first entry)
  (revised)
   95DE-01042702.
  96WO-EP004850.
  of present strand by
  Location/Qualifiers
  . 152
   69.0%;
  ā

 Mismatches

   Score 64.2; DB 3; Pred. No. 2.5e-10;
  complementary strand overhangs 3'
by sequence 5'-TCGA-3'"
   93
   18;
   Length
  Indels
   93
   0,
   Gaps
  60
   0
```

```
RRESULT 5
ADG48030
IID ADG4
XX
AC ADG4
XX
XX
AC ADG4
AC ADG4
XX
AC ADG4
AC ADG4
XX
AC ADG4
AC ADG4
AC ADG4
XX
AC ADG4
AC AD
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   CC The present sequence, which encodes a linker and the parathyroid hormone CC 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was CI ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains CC the Met(13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-CC PTH and the LacIq repressor plasmid pUBS500 were used to transform E. CC coli K12 RM82. The transformants were grown, with IPTG induction, in CC medium containing kanamycin and amplicilin. Cells were harvested, lysed CC and isolated inclusion bodies solubilised in guanidine hydrochloride, and CC renatured by dilution in pH 7 phosphate buffer. The solution was CC clarified and the supernatant concentrated and purified on a column of CC mombilised ininobiotin. The purified material was incubated with CC fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the CC fusion protein rapidly and completely, exclusively at the Lys residue in CC the linker, i.e. not at Lys residues in SA. (Updated on 25-MAR-2003 to CC correct PR field.)
  Matches
  Best Local
   Query Match
   thrombocytopaenia; megakaryocyte deficiency; platelet deficiency; thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia; metastatic tumours; systemic lupus erythematosus; aplenomegaly; Fanconi's syndrome; vitamin B12 deficiency; folic acid deficiency; May-Hegglin anomaly; Wiskott-Aldrich syndrome; paroxysmal nocturnal haemoglobinuria; glucagon-like peptide 1; GLP-1; non-insulin dependent diabetes; haemostatic; dermatological; immunosuppressive; antiinflammatory; cytostatic; mutant; variant;
  Example 2; Fig 2; 37pp; German.
  Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and parathyroid
  P-PSDB; AAW21946
  WPI; 1997-289290/26
   Sequence
   hormone production.
  Kopetzki E;
  Human PTH-TTR (C10A/K15A/G83C) variant fusion DNA
03-APR-2003; 2003US-00407078
   parathyroid
  Transthyretin; TTR; thrombopoietin mimetic peptide; TPO; TMP.
  11-MAR-2004 (first entry)
   ADG48030 standard; DNA; 489
   16-OCT-2003
  US2003195154-A1
  Synthetic
   linker, i.e. n
mect PR field.)
  97
  37
  62
  50;
   N
  Similarity
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  cuennucceaaaancecuecuecuecuecuecuecuecuecuecueaacuccauecaaaceue
  152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
  hormone;
  Conservative
   54.3%;
   dg.
   ; Score 52; DB 2; L6; Pred. No. 1.8e-06; 17; Mismatches 25;
   ВP
   128
  93
   Length 152;
   Indels
   0,
   Gaps
  96
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   The present invention relates to a method of increasing the serum half-CC life of a biologically active agent involves fusing the biologically CC active agent to transthyretin (TTR) or a TTR variant. The method is useful for increasing the serum half-life of a biologically active agent. CC Homogenous compositions comprising thrombopoietin (TPO) mimetic peptide CC (TMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet CC deficiency/thrombocytopaenia, dispathic thrombocytopaenia, megakaryocyte/platelet CC deficiency (Thrombocytopaenia, dispathic thrombocytopaenia, megakaryocyte/platelet CC e.g., aplastic anaemia, dispathic thrombocytopaenia, metastatic tumours CC which result in thrombocytopaenia, systemic lupus erythematosus, CC splenomegaly, Fanconi's syndrome, vitamin B12 deficiency, folic acid CC deficiency, May-Hegglin anomaly, Wiskott-Aldrich syndrome and paroxysmal CC nocturnal haemoglobinuria. Homogenous compositions comprising glucagon-CC like paptide 1 (CLP-1) is useful for treating non-insulin dependent CC diabetes. TMP compounds are useful in stimulating certain cell types CO other than megakaryocyte, which expresses Mp1 receptor and in maintaining CC the viability or storage life of platelets and related cells. The present CC sequence is human parathyroid hormone (PTH)-TTR variant fusion DNA.
  Query Match
Best Local S
Matches 47
   Transthyretin; TTR; thrombopoietin mimetic peptide; TPO; TMP; thrombocytopaenia; megakaryocyte deficiency; platelet deficiency; thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia; metastatic tumours; systemic lupus erythematosus; splenomegaly; Fanconi's syndrome; vitamin B12 deficiency; folic acid deficiency; May-Hegglin anomaly; Wiskott-Aldrich syndrome; paroxysmal nocturnal haemoglobinuria; glucagon-like peptide 1; GLP-1; immunosuppressive; antiinflammatory; cytostatic; mutant; variant; parathyroid hormone; PTH; ds.
   Increasing serum half-life of biologically active agent involves fusing biologically active agent to transthyretin or a transthyretin variant.
  04-APR-2002; 2002US-00117109
               US2003195154-A1
   Human PTH-TTR (C10A/K15A/A81C) variant fusion DNA.
   11-MAR-2004
  ADG48059 standard; DNA; 489
  Sequence 489 BP; 123 A; 128 C; 123 G; 115 T; 0 U; 0 Other;
   Example 3; SEQ ID NO 14; 61pp; English.
   WPI; 2004-051257/05
  Walker K, Xiong F;
  (WALK/) WALKER K. (XION/) XIONG F.
   65
   62
   ທ
  2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGUG
  l Similarity 47; Conser
   uugaauggcugcguaaaaaacugcaggacguu 93
   CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG
   TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
  Conservative
  (first entry)
  55.9%;
  20;
  ВÞ
  Score 52;
Pred. No.
  Mismatches
  DB 12;
  .3e-06;
les 25;
  Length 489;
   Indels
  ٥,
  Gaps
   64
   61
   0
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The present invention relates to a method of increasing the serum half-
CC life of a biologically active agent involves fusing the biologically
CC active agent to transthyretin (TTR) or a TTR variant. The method is
CC useful for increasing the serum half-life of a biologically active agent
CC Homogenous compositions comprising thrombocytopaenia, megakaryocyte/platelet
CC (TMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC (CTMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC e.g., aplastic anaemia, idiopathic thrombocytopaenia, metastatic tumours
CC which result in thrombocytopaenia, systemic lupus erythematosus,
CC splenomegaly, Fanconi's syndrome, vitamin B12 deficiency, folic acid
CC deficiency, May-Hegglin anomaly, Wiskott-Aldrich syndrome and paroxysmal
CC nocturnal haemoglobinuria. Homogenous compositions comprising glucagon-
CC like peptide 1 (GLP-1) is useful for treating non-insulin dependent
CC diabetes. TMP compounds are useful in stimulating certain cell types
CC ther than megakaryocyte, which expresses Mp1 receptor and in maintaining
CC the viability or storage life of platelets and related cells. The present
CC sequence is human parathyroid hormone (PTH)-TTR variant fusion DNA.
  Increasing serum half-life of biologically biologically active agent to transthyretin
   Walker K,
   04-APR-2002; 2002US-00117109
  03-APR-2003; 2003US-00407078
  Example 17; SEQ ID NO 43; 61pp; English.
   WPI; 2004-051257/05
  (XION/)
   16-OCT-2003
   Xiong F;
  active agent involves fusing or a transthyretin variant.
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   Query Match
Best Local 9
  Matches
65
          62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                  ഗ
  2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
  1 Similarity
47; Conserv
TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
                                Conservative
  55.9%;
  20;
  Score 52; DB:
Pred. No. 2.3e:
20; Mismatches
  ина
2.3e-06;
25;
   DB 12;
   Length 489;
  Indels
  0
   Gaps
                                    64
   61
```

Sequence 489 BP; 123 A; 128 C; 123 G; 115 T; 0 U; 0 Other;

```
RESULT 7
ADDG678
ADDG678
ADDG678
AC ADGG
AC AC ADGG
AC ADGG
AC ADGG
AC ADGG
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AC ADGG
AC
  ADG68786 standard; cDNA; 489
```

Human mutant transthyretin (TTR) CDNA #12.

11-MAR-2004

(first entry)

Human; transthyretin; TTR; gene; ss; TPO mimetic peptide; TMP; thrombocytopenia; aplastic anaemia; metastatic tumour; cancer; haemostatic; antianaemic; cytostatic; mutant

US2003191056-A1 Homo sapiens.

```
RESULT 8
ADG93179
ID ADG9
XX ADG9
AC ADG9
XX ADG9
XX NOVE
XX NOVE
XX NOVE
XX UNic
PN WO2(
XX Unic
PN WO2(
XX Unic
PN WO2(
XX Unic
XX U
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   Query Match
Best Local
  biologically active agent comprising fusing the agent to transthyretin (TTR) or a TTR variant. The invention also relates to a homogenous preparation of a TTR-biologically active agent fusion, a TTR variant-biologically active agent fusion, a TTR variant-biologically active agent fusion, a TTR variant-biologically active agent fusion and a PEG-TTR variant-biologically active agent fusion and pharmaceutically acceptable diluent, carrier or adjuvant. The method is used to increase the serum half-life of a biologically active agent, e.g. a protein or a peptide. A preparation comprising a TPO mimmetric peptide (TMP) is used to treat thrombocytopenia, aplastic anaemia and metastatic tumours. This sequence represents cDNA encoding a human mutant TTR polypeptide of the invention.
   Increasing the serum half-life of a biologically active agent for treating thrombocytopenia, comprises fusing the agent to transthyretin a variant of it.
  expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body; gene; ds.
  ADG93179 standard; DNA; 102
   Sequence 489 BP; 123 A; 128 C; 123 G; 115 T; 0 U; 0 Other;
   The invention relates to a method for increasing the serum half-life of
  Example 3; SEQ ID NO 14; 35pp; English
  Walker K, Xiong F;
  04-APR-2002; 2002US-00117109
  04-APR-2002; 2002US-00117109
   Unidentified
  Novel expression cassette-related polypeptide-encoding DNA SeqID60.
  11-MAR-2004
   (WALK/) WALKER K. (XION/) XIONG F.
                                Harley S,
   24-MAY-2002; 2002US-0383370P
  23-MAY-2003; 2003WO-US016643
  WO2003100021-A2
   (REST-) RESTORAGEN INC. (HARL/) HARLEY S.
   2004-010111/01
   65
   62
  ហ
   N
  Similarity
   TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
   Williams JA,
   Conservative
   (first entry
  55.9%; Score 52; DB 12;
51.1%; Pred. No. 2.3e-06;
tive 20; Mismatches 25
                                    Luan
                                    ָש,
  Length 489;
   Indels
   64
  ဝူ
   0
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RESULT 9
ADJ65857
  밁
밁
   S
  á
   Query Match
Best Local 8
  Matches
  This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
  WPI; 200
P-PSDB;
  Sequence
  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   06-MAY-2004
  Disclosure; SEQ ID NO 60; 157pp; English.
   P-PSDB; ADG93159.
   WPI; 2004-035128/03.
   expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
  Xia Y,
  24-MAY-2002; 2002US-0383212P
   23-MAY-2003; 2003WO-US016645
  04-DEC-2003
   WO2003100022-A2
   PTH peptide coding sequence
   ADJ65857 standard; DNA; 102
   (REST-) RESTORAGEN INC.
  Local Similarity 52.2
les 48; Conservative
   2004-035129/03.
DB; ADJ65837.
   N
  2 CUGUTUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
   Peng L;
   UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
  102 BP; 30 A; 24 C; 22 G;
   TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   SEQ ID NO 33; 132pp; English.
   (first entry)
   54.2%;
  18;
   #1
  Score 50.4; DB 1:
Pred. No. 5.1e-06,
8; Mismatches 20
  26 T; 0 U; 0 Other;
   DB 12;
  93
  93
   Length
   Indels
  0
  Gaps
  61
   0
```

expression cassette of the invention

or R

```
RESULT 10
ADW14377
ID ADW14
XX ADW14
AC ADW14
AC Human
XX Homo
XX Homo
XX Homo
XX 12-DE
XX 12
g
                                 Ś
   밁
   δ
  유
  В
  δ
   ភិនិស្សន្តន្ទ
  Query
Best L
  Matches
  Query Match
Best Local
   Matches
   The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-Pro 1-34 peptide (ADW14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the PTH 1-34 peptide.
   polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
  Sequence 102 BP; 30
  Sequence 102 BP; 30 A; 24 C;
   Disclosure; SEQ ID NO 3; 25pp; Chinese.
   12-DEC-2001; 2001CN-00142627
   CN1424325-A.
   Homo sapiens
   ds; parathyroxin;
  Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3
   10-MAR-2005
   ADW14377;
  ADW14377 standard;
   Production of reorganized human parathyroid hormone 1-34 peptide
   (SHAN-)
  12-DEC-2001; 2001CN-00142627.
  18-JUN-2003.
   Match
Local (
  2004-099606/11.
DB; ADW14378.
62
   62
  62
  62
   48;
   N
   N
  N
  N
  48;
   Similarity
  SHANGHAI BIOLOGICAL ENG
  Similarity
::|||:|||:|||:|||:|||||:::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
   ::|||:|||:|||:|||:|||||::|||:::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                            UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUCGUCUGAACUCCAUGGAACGUG 61
   Xiu C,
  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
  Conservative
   Conservative
   Ľ
  recombinant
  DNA;
   3
  A; 24 C;
  entry)
  54.2%;
   54.2%;
   102
   18;
  18;
   Score 50.4; DE
Pred. No. 5.1e-
18; Mismatches
   ВÞ
  Score 50.4; DB 12;
Pred. No. 5.1e-06;
8; Mismatches 26;
  22 G; 26 T; 0 U; 0 Other;
  22 G;
  protein;
  RES
  26 T;
  CENT
  protein
   5.1e-06;
nes 26;
  0 U;
  ACAD
93
  DB
   93
  13;
  0
  engineering
  Other;
   Indels
  Length
   Length
  Indels
  102;
  102;
  0;
  0
  Gaps
  Gaps
   61
   61
  61
  0
```

RESULT 12
ADJ65858
ID ADJ6
XX
AC ADJ6
XX
DT 06-N
XX
DE PTH

ADJ65858; ADJ65858

standard;

DNA;

111

ВР

61 61 0

PTH peptide 06-MAY-2004

coding sequence

#2

(first

entry)

```
ADG931MT 11
ADG93
ID ADG93
XX ADG93
XX ADG93
XX I11-N2
XX WC20
XX Unide
XX 
                                      5
   밁
   5
밁
  Query Match
Best Local S
Matches 48
  This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The producing peptide and inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
   New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
   Unidentified
  Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
   Disclosure; SEQ ID NO 61; 157pp; English
  Harley S,
  24-MAY-2002; 2002US-0383370P
  04-DEC-2003
  WO2003100021-A2
  Novel expression cassette-related polypeptide-encoding
   11-MAR-2004
  P-PSDB; ADG93160.
   (REST-)
(HARL/)
  23-MAY-2003; 2003WO-US016643
  tandem
   ADG93180 standard; DNA; 111
   2004-035128/03
62
  62
  N
   N
   48;
   polypeptide;
   RESTORAGEN INC
HARLEY S.
  Similarity
                           UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
  CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  Williams
  cassette;
   Conservative
   (first
   ; high yield polypeptide production, inclusion body; gene; ds.
  54.2%; Score 50.4; DB 12
52.2%; Pred. No. 5.2e-06;
tive 18; Mismatches 26
   Luan
   ВP
   ď
   Xia
  DB 12;
93
   26;
  Length
   Indels
   DNA
   111;
   0
   Gaps
```

```
RESULT 13
ADW14375
ID ADW14
XX ADW14
XX ADW14
XX IO-MA
AC Human
AX Human
AX Human
AX Homo
AX Homo
AX Homo
AX Homo
AX Homo
AX IS-DE
  밁
   5
  밁
  á
  Query Match
Best Local (
   polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
  04-DEC-2003
   expression cassette; tandem polypeptide; inclusion inclusion body fusion partner; PTH; gene; ds.
  Sequence 111
   Disclosure; SEQ ID NO 34; 132pp; English.
  sequence, useful for producing a tandem polypeptide that forms
inclusion body when expressed in a cell.
   New expression cassette comprising an operably linked nucleic acid
  P-PSDB; ADJ65838.
  WPI; 2004-035129/03.
   Xia Y,
  24-MAY-2002; 2002US-0383212P
   23-MAY-2003; 2003WO-US016645
   WO2003100022-A2
   Unidentified
  The invention comprises an expression cassette which produces
  12-DEC-2001; 2001CN-00142627
   CN1424325-A.
  ds; parathyroxin;
   Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
   10-MAR-2005
  ADW14375 standard; DNA; 111
  18-JUN-2003
  (SHAN-) SHANGHAI BIOLOGICAL ENG
  sapiens
   62
   62
   N
  N
  48;
   Peng
  RESTORAGEN INC.
  Similarity
  UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
  cugurucceaaaauceguegueguegueguegueguegucueaacuccauegaaceue 61
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  Conservative
                          2001CN-00142627.
   BP; 30
  (first
  recombinant protein; protein engineering
   ₽
  entry)
   54.2%;
   26 C;
   ; Score 50.4; I
; Pred. No. 5.26
18; Mismatches
   25
   <u>ი</u>
  RES
   30 T; 0 U;
  CENT ACAD
  2e-06;
   DB 12;
   26;
   0 Other;
   Indels
   Length
   body;
  oduces a tandem in a cell. The
   0
  an
   Gaps
  61
   0
```

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   á
  밁
   Ş
  Matches
  Query Match
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   parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the Gly-Ser-Pro-PTH 1-34 peptide.
   Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;
  Claim 3; SEQ ID NO 1; 25pp; Chinese.
   Production of reorganized human parathyroid hormone 1-34
  New expression cassette comprising an operably linked nucleic sequence, useful for producing a tandem polypeptide that forms inclusion body when expressed in a cell.
   11-MAR-2004
   ADG93260
  expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body; gene; ds; PTH.
  Novel expression cassette-related
  Disclosure;
   WPI; 2004-035128/03.
P-PSDB; ADG93259.
  Harley S, Williams
  24-MAY-2002; 2002US-0383370P
  23-MAY-2003; 2003WO-US016643
  04-DEC-2003.
   WO2003100021-A2
  Synthetic
  Unidentified
  (HARL/)
  (REST-)
   ocal Similarity
  C
   2004-099606/11.
   11
  71
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  48;
   N
   polypeptide;
  RESTORAGEN
HARLEY S.
   ADW14376
  standard;
   CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
   Xiu
  TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102
  SEQ ID NO 141; 157pp;
   (first entry)
  Conservative
   ú
   Ŀ
  INC.
  DNA;
   54.28;
  117
  Luan
  18;
  ВP
  Score 50.4; DB 13;
Pred. No. 5.2e-06;
8; Mismatches 26;
  שֻ
  English.
  PTH DNA SeqID141.
  Xia
  Indels
  Length
   peptide
   0
   Gaps
   61
  70
  0
```

This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette

SSSSSSSSS

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RESULT 15
AART34865
AART34865;

AC
AART34865;

XX
O2-DEC-1996 (first entry)
XX
Plasmid pBN1: pTH (1-34)C-1c port
XX
PTH; parathyroid hormone; parat
XX
PTH; parathyroid pBN1; carbonic
XX
PDH; parathyroid pBN1; carbonic
XX
Synthetic.

XX
VC
PTH; parathyroid pBN1; carbonic
XX
VC
PTH; product= "hCA-
XX
PD 13-JUN-1996."
XX
PTH; product= "hCA-
XX
PD 13-JUN-1996."
XX
PTH; parathyroid
PTH; production of C-terminal alphanic
PTH; production of C-terminal pph; carbonic anhydrase II joined by constructs.
XX
PD 13-JUN-1996."
XX
PR P-PSDB; parathydrase II joined by constructs.
XX
PD 2 Example 7; Fig 1; 93pp; Englisl
XX
PD 2 Carbonic anhydrase II joined by constructs.
XX
PD 2 Carbonic anhydrase II joined by constructs.
XX
PD 3 Cys residue and C-terminal constructs.
XX
PD 4 Cys residue enable th constructs.
XX
PD 5 Carbonic anhydrase II joined by constructs.
XX
PD 6 Carbonic anhydrase II joined by constructs.
XX
PD 1 Carbonic anhydrase II joined by constructs.
XX
PD 1 Carbonic anhydrase II joined by constructs.
XX
PD 1 Carbonic anhydrase II joined by constructs.
XX
PD 1 CR 2 PRIB; PS  Query Match
Best Local S
Matches 48
  produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferable at tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a PTH peptide which was used in the exemplification of the invention.
   A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding for a fusion protein (AAR87867) composed of the C-terminal end of human carbonic anhydrase II joined by an intraconnecting peptide (including a thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in E. coli transformants. The intraconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be selectively reacted to produce C-terminal carboxamidated PTH(1-34)
  PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide; alpha-carboxamide; recombinant protein; fusion protein; transpeptidation; vector; plasmid pBN1; carbonic anhydrase II; ss.
   Example 7; Fig 1; 93pp; English.
   Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage and transpeptidation of recombinant multicopy peptide(s) or fusion
  Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||||::
62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
   48;
   N
   2 cucurucceaaaauceeuceuceuceuceuceuceuceuceuceaacuccauceaaceuc 61
   h 54.2%;
Similarity 52.2%;
48; Conservative 1
   pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
   Location/Qualifiers
  /*tag= a
/product= "hCA-linker-PTH(1-34)Cys fusion"
  Heriksen DB,
   18;
   Score 50.4; DB 12
Pred. No. 5.3e-06;
8; Mismatches 26
  ВP
  Holmquist B,
  DB 12;
  Length 117;
   Indels
  Wagner FW;
   0;
   Gaps
   61
   0
```

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유
                                       Вb
   SS
   δ
  Query Match
Best Local S
Matches 48
   Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;
62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||::
107 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 131
   47
  N
   Similarity
  CUGUUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGUG
  Conservative
  54.2%;
   Score 50.4; DB 2;
Pred. No. 5.7e-06;
8; Mismatches 26;
   138
   Length 168;
   0
   Gaps
  106
  61
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Search completed: November 23, Job time: 243.667 secs

2005, 23:00:15

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   Maximum
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   9.
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and is derived by analysis of the total score distribution.
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  93
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| 45                 | 44       | 43       | 42       | c 41     | 40       | c 39     | c 38     | 37                 |                    | c 35              |                    | 33                 | 32                 | c 31               | 30       | c 29     | 28     |                    | c 26     | c 25     | 24       | 23       |
|--------------------|----------|----------|----------|----------|----------|----------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------|--------------------|----------|----------|----------|----------|
| 34                 | 34       | 34       | 34       | 34.2     | 34.2     | 34.4     | 34.6     | 34.6               | 34.8               | 34.8              | 35                 | 35                 | 35.4               | 35.6               | 35.6     | 35.8     | 36.2   | 36.6               | 36.6     | 36.6     | 37.2     | 38.2     |
| 36.6               | 36.6     | 36.6     | 36.6     | 36.8     | 36.8     | 37.0     | 37.2     | 37.2               | 37.4               | 37.4              | 37.6               | 37.6               | 38.1               | 38.3               | 38.3     | 38.5     | 38.9   | 39.4               | 39.4     | 39.4     | 40.0     | 41.1     |
| 650                | 605      | 562      | 550      | 744      | 514      | 501      | 1013     | 972                | 939                | 301               | 705                | 540                | 509                | 570                | 417      | 844      | 339    | 766                | 620      | 575      | 316      | 820      |
| ທ                  | σı       | ഗ        | ഗ        | 7        | 9        | 2        | 10       | 10                 | 10                 | 11                | ۳                  | N                  | 7                  | _                  | 9        | σ        | œ      | _                  | σ        | ۲        |          | 5        |
| BU008102           | BQ861241 | BU005353 | BQ987803 | CK481107 | BZ137695 | BE360066 | CW921961 | CNS02QMI           | CG442723           | CR159040          | AI031553           | BE212803           | CO984533           | AA771739           | CC894877 | CA184654 | T29548 | AA843141           | CF231132 | AA772070 | AA372113 | BX103059 |
| BU008102 QGH6I04.y |          | -        |          |          |          |          | -        | AL209475 Tetraodon | CG442723 OGFAU171V | CRISUAU FORWARD S | AI031553 0W48C08.X | BE212803 IpBrn0085 | CO984533 GM8901382 | AA771739 a132e09.8 |          |          |        | AA843141 aK06C02.8 |          |          |          |          |

## ALIGNMENTS

RESULT 1 AI909008 LOCUS REFERENCE AUTHORS VERSION KEYWORDS FEATURES COMMENT ACCESSION DEFINITION JOURNAL ORGANISM PUBMED source Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=QV&t2=QV-BT197-038.html
&t3=050499&t4=1) Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research Shotgun sequencing of the human transcriptome with ORF Hominidae; Homo.

1 (bases 1 to 527)

1 (bases 1 to 527)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens QV-BT197-050499-038 BT197 sequence tags AI909008.1 GI:6499688 Fax: +55-11-2707001 Tel: +55-11-2704922 lomo sapiens (human) primer: puc 18 forward. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) /dev\_stage="Adult" /clome\_lib="BT197" /note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: /organism="Homo sapiens"
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41.1 41.1 41.1 41.1 41.1 41.1

AA788985 BG198564 AI051997

W56120 zc55h06.r1
W39202 zb35h03.r1
AA788985 ah29c05.s
BG198564 RST17829
A1051997 cy29c05.x
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W52945 W19765 W52795

W56820

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Query Match
Best Local
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32; Conservative
  Hominidae; Homo.

1 (bases 1 to 324)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Tan,F.,

Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
Seq primer: mob.REGA+ET
High quality sequence stop: 222.
   Unpublished (1995)
Contact: Wilson RK
   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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   W19763
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IMAGE: 05552 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
  The WashU-Merck EST Project
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//note="Organ: parathyroid_gland; Vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
   Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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9; Mismatches 3;
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  ORIGIN
  밁
   ş
          Query Match
Best Local Similarity
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT W19763

N

LOCUS DEFINITION

밁 5

REFERENCE AUTHORS

COMMENT

TITLE JOURNAL

FEATURES

41.18;

Score Pred.

38.2; DB No. 0.61;

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TITLE
JOURNAL
COMMENT
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Matches 33
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  42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCAGGACGU 92
100 TCTGAACTCGATGGAGGAGGAGTTGGTTGCGTAAGAANCTGCAGGATGT 150
  Unpublished (1995)
Contact: Wilson RK
Contact Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
   Hominidae; Homo.

1 (Dases 1 to 352)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Hillier,L., Luttman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  W39062

Zb34c06: rl Soares parathyroid tumor NbHPA Homo sapiens cDNA colone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN); mRNA sequence.
   th 41.7%; similarity 64.7%; 33; Conservative 1
   Homo sapiens (human)
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
  The WashU-Merck EST Project 
Unpublished (1995)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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10;
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   ŏ
   0
   Gaps
  0
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REFERENCE
AUTHORS
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  RESULT
W38966
  ACCESSION
VERSION
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  SOURCE
   KEYWORDS
  DEFINITION
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  Matches
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  4
   225
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   42 UCUGAACUCCAUGGAACGUGUUGAAAUGGCUGCGUAAAAAAACUGCAGGACGU
  42
  w38966
zb28b12.r1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE.304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
  33,
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
  4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
   The WashU-Merck EST Project Unpublished (1995)
Contact: Wilson RK
  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
   W38966.1
  Seq primer: mob.REGA+ET
  Hominidae; Homo.
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Eukaryota;
  Homo sapiens (human)
   (HUMAN);, mRNA sequence.
  Similarity
   TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 275
                              :|:||||:| |:||| |: ||: ||:||:||:||:|| |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
  UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   (bases 1 to 376)
   sapiens
  Conservative
  Conservative
   TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
  /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
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/note="Organ: parathyroid_gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco_RI; 1st strand_cDNA_was_primed_with a Not I -
   GI:1320674
  Location/Qualifiers
  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248305"
  clone="IMAGE:304895"
   Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  xref="taxon:9606"
  41.1%;
  10;
  Score 38.2; D
Pred. No. 0.62
10; Mismatches
   Mismatches
  .62;
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  Louis,
   Length 376;
   Indels
   Indels
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   EST 15-MAY-1996
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   0
  92
  Gaps
  Gaps
   0
  0
   JOURNAL COMMENT
   REFERENCE
AUTHORS
   VERSION
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W31998
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   ORIGIN
   FEATURES
   ACCESSION
  DEFINITION
   ORGANISM
   Best Local
Matches
  Query Match
   source
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   42
   1 Similarity
33; Conserv
  Unpublished
   Homo sapiens
  TSE
   W37708.1
      W31998
   Wilson, R.
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mRNA

linear

EST 20-AUG-1996

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250 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300
   w37708 All bp mRNA linear EST 10-OCT-199 zc10d12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE 321911 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   Hominidae; Homo.

1 (bases 1 to 41)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 876 Std Error: 0.00
   Tel: 314 286 1800 Fax: 314 286 1810
   The WashU-Merck EST Project 
Unpublished (1995)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  High quality sequence stop: 396
  Washington University School of Medicine
  Contact: Wilson RK
   Homo sapiens (human)
   Seq primer: mob.REGA+ET
   Email: est@watson.wustl.edu
  HUMAN);, mRNA sequence.
   ucugaacuccauggaacguguugaauggcugcguaaaaaacugcagacgu 92
  Conservative
   /lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares parathyroid_tumo_NbHPA"
/clone lob="Soares parathyroid_state_not parathyroid_plane, vector: pT7T3D
/note="Organ: parathyroid_gland, vector: pT7T3D
(pharmacia) with a modified polylinker; Site_1:
Site_2: Eco RI; lst strand cDNA was primed with
   TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cct = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
  GI:1319302
  /tissue_type="parathyroid tumor"
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/mol_type="mRNA"
  ocation/Qualifiers
  41.1%;
   10;
  Score 38.2; DB pred. No. 0.63;
  Mismatches
  8
  Louis,
  Length 411;
  Wohldmann, P. and
   Indels
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   contact the
   Marra, M.,
   EST 10-OCT-1996
  0
   Not I;
  Gaps
   0
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AUTHORS
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   DEFINITION
  Query Match
Best Local S
Matches 33
  ORGANISM
  Hominidae; Homo.

(bases 1 to 416)

(bases 1 to 416)

Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chispes, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hiltman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Le, M., Hawkins, M., Hiltman, M., Worris, M., Parsons, J., Prange, C., Rifkin, L., Mardis, E., Moore, B., Morris, M., Barsons, J., Prange, C., Rifkin, L., Mardis, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
  W31998 W31998.1 GI:1313010 EST.
  zb96d06.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
(HUMAD);, mRNA sequence.
W38764 434 bp mRNA linear EST 15-MAY-1996 zb27a07.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
   Generation and analysis of 280,000 human expressed sequence tags
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homo sapiens (human)
   Similarity
  41.1%; ilarity 64.7%; Conservative 1
   quality
   /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="modb.1258309"
/db_xref="rodb.1258309"
/db_xref="rodb.1258309"
/db_xref="taxon:9606"
/clone="IMAGE:20651"
/tissue type="parathyroid tumor"
/lab_host="purpl0B (ampicillin resistant)"
/lab_host="purpl0B (ampicillin resistant)"
/clone=lib="soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pi773D
/note="Organ: parathyroid gland; Vector pi773D
/note="Organ: parathyroid g
   ity sequence stop: 386.
Location/Qualifiers
   10;
  Score 38.2; DB 8;
Pred. No. 0.63;
0; Mismatches 8;
  8;
   Length 416;
   Indels
  0,
   Gaps
   0
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AUTHORS
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VERSION
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   TITLE
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Matches 33
   214
   42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU
                W56235
W56235.1
EST.
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 253.
Location/Qualifiers
  W56235
zc01e11.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone image:321068 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   The WashU-Merck EST Project Unpublished (1995)
Contact: Wilson RK
   li (bases 1 to 434)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Tel: 314 286 1800
Fax: 314 286 1810
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Hominidae; Homo.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  W38764
W38764.1
  IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
   Similarity 64.
  (HUMAN);, mRNA sequence.
   /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)
/lab_host="DH10B (ampicillin
   /organism="Homo sapiens"
/mol type="mRN"
/db xref="GDB:1248198"
/db xref="taxon:9606"
/clone="IMAGE:304788"
   41.1%;
   10;
   Score 38.2; D
Pred. No. 0.63
LO; Mismatches
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.63;
   8;
   8,
   Length 434;
   Indels
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Marra, M.,

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   ACCESSION
  ORGANISM
   Matches
   Query Match
   ORGANISM
   source
   Local
  42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
  W33077
W33077.1
   W33077

453 bp mRNA linear EST 10-OCT-1990 c0707a12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE.321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
  Hominidae; Homo.

1 (bases 1 to 450)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Homo
   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 865 Std Error: 0.00
  Tel: 314 286 1800
Fax: 314 286 1810
  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
   Unpublished (1995)
Contact: Wilson RK
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Email: est@watson.wustl.edu
   The WashU-Merck EST Project
   Wilson, R.
  Homo sapiens (human)
  Hominidae; Homo.
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Homo sapiens
  Homo sapiens (human)
   Similarity
  primer: mob.REGA+ET
  sapiens
   Conservative
   TTTTT-3'], double stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fattima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
   /clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid_gland; Vector: pT7T3D
/Pharmacial with a modified_polylinker; Site 1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
   /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
  Location/Qualifiers
  GI:1315062
   mRNA sequence.
   mol_type="mRNA"
db_xref="GDB:1258726"
   organism="Homo sapiens"
  clone="IMAGE:321068"
  xref="taxon:9606"
   41.1%; Score 38.2; DB 8; 64.7%; Pred. No. 0.63;
   10;
   Mismatches
   8
   Length 450;
  Indels
  Marra,M.,
  EST 10-OCT-1996
   0;
   Gaps
  0
   ACCESSION
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AUTHORS
   REFERENCE
AUTHORS
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  rocar
   42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU
   1 (bases 1 to 453)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Mammalia; Eutheria; Euarchontoglires;
Hominidae; Homo.
1 (bases 1 to 496)
1 (bases 1 to Lark, N., Dubuque, T., Elli
Hillier, L., Clark, N., Kucaba, T., Le, M., Rohlfing, T., Sc
   zc01a03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
   High quality sequence
  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 871 Std Error: 0.00
  Tel: 314 286 1800
Fax: 314 286 1810
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Unpublished
  The WashU-Merck EST Project
  Homo sapiens
   EST
  W56820
  Email: est@watson.wustl.edu
  Contact: Wilson RK
  Eukaryota; Metazoa; Chordata;
   Homo sapiens (human)
   W56820.1
  (HUMAN);,
  Similarity
   primer: mob.REGA+ET
   Conservative
  /clone lib="Soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
/pharmacia) with a modified polylinker; Site 1:
Site 2: Eco RI; 1st strand cDNA was primed with
oligo(dT) primer
  /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
   /mol_type="mRNA"
/db_xref="GDB:1259256"
/db_xref="taxon:9606"
  mRNA sequence.
   GI:1358743
   clone="IMAGE:321598"
  organism="Homo sapiens'
   ocation/Qualifiers
  .453
  (1995
  41.1%;
   10;
  Score 38.2; DB Pred. No. 0.63; 0; Mismatches
   stop: 367.
   496 bp
   Craniata; Vertebrata; Euteleostomi; oglires; Primates; Catarrhini;
                       Elliston, K., Hawkins, M.,
Le, M., Lennon, G., Marra, M.,
  DB 8;
  8
  Length 453;
   Indels
   linear
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Gaps

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   RESULT 11
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  Query Match
Best Local S
Matches 33
                        TITLE
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  source
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  l Similarity
33; Conserv
  Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashUnerck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
14444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
The WashU-Merck EST Project 
Unpublished (1995)
  Hominidae; Homo.

1 (bases 1 to 523)

1 (bases 1 to 523)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  W52945 523 bp zc03h08.rl Soares parathyroid to IMAGE: 321279 5' similar to gb:V0
   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 858 Std Error: 0.00
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   Homo sapiens (human)
   (HUMAN);, mRNA sequence.
W52945
  Insert Length: 858 Sto
Seq primer: mob.REGA+ET
   W52945.1 GI:1350379
  quality sequence
  Conservative
   TTTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Banto Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258662"
/db_xref="taxon:9606"
  rty sequence stop: 424.
Location/Qualifiers
   . 496
   41.1%; Score 38.2; DB 8; 64.7%; Pred. No. 0.64; tive 10; Mismatches 8;
  old tumor NbHPA Homo sapiens cDNA clone gb: V00597 PARATHYROID HORMONE PRECURSOR
   mRNA
  8;
  Length 496;
   linear
   Marra, M.,
  EST 10-OCT-1996
  0;
  Gaps
  0
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JOURNAL
COMMENT
   REFERENCE
AUTHORS
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  DEFINITION
   KEYWORDS
  Matches
  Query Match
Best Local Similarity
  ORGANISM
   39
  42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
   33,
   Hominidae; Homo.

1 (bases 1 to 536)

1 (bases 1 to 536)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Kucaba, T., Le, M., Lennon, G., Marra, M. Holman, M., Hultman, M., Kucaba, T., Soares, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Parkway, Box 8501, St. 1 Tel: 314 286 1800
   M19765 W19765 DARAY-1996 TRNA linear EST 03-MAY-1996 zb39c03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:305956 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN); mRNA sequence.
   Homo sapiens (human)
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   W19765.1 GI:1295882
  Conservative
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Marra, M.,

```
Contact: Wilson RK
Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
   This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further i Insert Length: 702 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 304.
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41.1%; Score 38.2; 164.7%; Pred. No. 0.69; ive 10; Mismatches
   School of Medicine
vay, Box 8501, St. Louis,
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                  8
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   information.
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JOURNAL COMMENT
   REFERENCE
AUTHORS
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W52795
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  KEYWORDS
  DEFINITION
   VERSION
  ACCESSION
   Matches
   Query Match
   ORGANISM
  Best Local
  TITLE
   source
  229 TCTGAACTCGATGGAGAGAGAGATGGCTGCGTAAGAAGCTGCAGGATGT 279
  ω
ω
   Hominidae; Homo.

1 (bases 1 to 547)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
  zc02b12.rl Soares parathyroid IMAGE:321119 5' similar to gb
  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
   The WashU-Merck EST Project Unpublished (1995)
Contact: Wilson RK
     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 651 Std Error: 0.00
  Tel: 314 286 1800
Fax: 314 286 1810
  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homo sapiens
  W52795.1 GI:1350435
   Homo sapiens (human)
  Similarity
  (HUMAN);, mRNA sequence.
   314 286 1810
   quality sequence stop: 352.
   Conservative
Length:
  est@watson.wustl.edu
  TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
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/lab host="DH10B (ampicillin resistant)"
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/note="Organ: parathyroid gland; Vector: pT773D
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   Williamson, A., Wohldmann, P. and
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   EST 10-OCT-1996
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ACCESSION
VERSION
KEYWORDS
  REFERENCE
AUTHORS
  RESULT 14
W56120
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  COMMENT
  SOURCE
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   ORIGIN
   FEATURES
   DEFINITION
   Locus
                     FEATURES
   Matches
   Query Match
   Best Local
   TITLE
  ORGANISM
   JOURNAL
   source
source
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W56120.1
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   The WashU-Merck EST
Unpublished (1995)
Contact: Wilson RK
   Hominidae; Homo.

1 (bases 1 to 576)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
   W56120 576 bp mRNA linear EST 11-OCT-199 zc56h06.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810

Fax: 314 286 1810
  Seq primer: mob.REGA+ET
   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Insert Length: 904 Std Error: 0.00
   Seq primer: mob.REGA+ET
   Homo sapiens (human)
                                       High quality sequence stop: 433
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   (HUMAN);, mRNA sequence.
   quality sequence
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   TTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
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   _type="mRNA"
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  Mismatches
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  Louis, MO 63108
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   Marra, M.,
   EST 11-OCT-1996
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TITLE
JOURNAL
COMMENT
  REFERENCE
AUTHORS
   ACCESSION
VERSION
   KEYWORDS
   DEFINITION
  Query Match
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Matches 33
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   224 TÉTGAACTÉGATGGAGAGAGTAGAATGGETGCGTAAGAAGETGEAGGATGT 274
   42
   The MashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
   Hominidae; Homo.

1 (bases 1 to 583)

1 (bases 1 to 583)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
   w39202 583 bp mRNA linear EST 15-MAY-199
zb35h03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:3056215; similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
  W39202
W39202.1
  h 41.1%; Score 38.2; DB 8; Length 576; Similarity 64.7%; Pred. No. 0.66; 33; Conservative 10; Mismatches 8; Indels
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  (HUMAN);, mRNA sequence.
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RESULT W39202

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ORIGIN

ORIGIN

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Sequence 132, App
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Perfect score:
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   Run on:
  Result
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```
APPLICANT: Jung, Bun-Kyung
APPLICANT: Jung, Bur-Kyung
APPLICANT: Dark, Doo-Hong
APPLICANT: Chung, Soo 11
TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
FILE REFERENCE: 0136/06266
CURRENT APPLICATION NUMBER: US/09/463,282D
CURRENT FILING DATE: 1998-00-1-20
PRIOR PAPLICATION NUMBER: PCT/KR98/00146
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1999-00-01-20
RIOR PRILING DATE: 1999-00-05
RIOR PLILING DATE: 1999-00-05
RIOR PLILING DATE: 1997-01-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Version 3.1
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IS-08-142-551B-132/C
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| Patent No. 5844603
| GENERAL INFORMATION:
| APPLICANT: Oldenburg, Kevin R.
| APPLICANT: Oldenburg, Kevin R.
| TITLE OF INVENTION: COMPOUNDS WITH PT |
| TITLE OF INVENTION: RECOMBINANT DNA V, NUMBER OF SEQUENCES: 132
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Matches 47; Conservative
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APPLICATION NUMBER: US/08/468,275
[TILING DATE: 06-JUN 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELEPONE: (415) 496-8150
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 141 base pairs
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   (415) 496-8150
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25
  NAME/KEY: CDS
LOCATION: 7..138
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   RESULT 4
US-08-468-275-5/c
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18-Gequence 3. Application US/08468275
18-GENERAL INFORMATION:
18-DELEAUT: HOLLADAY, LESLIE A.
18-DELEAUT: HOLLADBURG, KEVIN R.
18-DELEAUT: HOLLADBURG, KEVIN R.
18-DELEAUT: OLDENBURG, KEVIN R.
18-DELEAUT: OLDENBURG, KEVIN R.
18-DELEAUT: OLDENBURG, RETURN R.
18-DELEAUT: OLDENBURG, LOSPERSEN IO CORRESPONDENCE ADDRESS:
10-DERESSEE: ALZA CORPORATION
2TREET: 950 PAGE MILL ROAD
   COUNTRY:

ZIP:
COUNTRY:
COUNTRY:
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COMPUTER READABLE FORM:
COMPUTER:
COMPUT
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COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
           CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Sw
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
  TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
   : 74 base pairs
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EDNESS: single
  STREET: 950 CITY: PALO ALTO
  STRANDEDNESS:
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Query Match

49.7%; Score 46.2; DB 2; Length 141;
Best Local Similarity 51.6%; Pred. No. 4.8e-05;
Matches 47; Conservative 16; Mismatches 28; Indels
  Sequence 5, Application US/08468275
Sequence 5, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLDENBURG, KEUN R.
TITLE OF INVENTION: BLECTROTRANSPORT FLUX OF POLYPEPTIDES
INVENTION: APPLICANT SECONDAICS ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSERE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CONTRIBUTION: STREET: S
  COUNTRY: PALLY CALLY COUNTRY: CALLY CONTRY: CALLY CONTRY: CALLY CONTRY: CALLY CONTRY: CALLY CONTRY: CALLY CONTRY: CALLY CONTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Determine PC-DOS/MS-DOS
SOFTWARE: Determin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: OG-JUN 1995
CLASSIFICATION: DATA:
ATTONIEY/AGAIT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 0366-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
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28; Indels
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FILING DATE:
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   Sequence 3, Application US/08952980B
Patent No. 6333189
  DNA (genomic)
  COUNTRY: USA
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  linear
  TOPOLOGY: 11
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 Matches
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  2 CUGUIUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCGAACUCCAUGGAACGUG 61
  ö
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  Sequence 3, Application US/09007466
Patent No. 6313092
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: CLUEBENGY, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
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   NUMBER OF SEQUENCES: 10
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ADDRESSE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
CITY: PALO FOR MILL ROAD
CITY: USA
ZIP: 94303-0802
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATE: IBM PC compatible
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SOFTWARE: DATENTING SYSTEM: VO-DOS/NS-DOS
SOFTWARE: USA
STATE: USA
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/007,466
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FILING DALE:
FILING APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,275
FILING DATE: 06-4UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REGISTRATION NUMBER: 30,661
FELEPACOMMULICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8150
INFORMATION FOR EG ID NO: 3:
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51.6%;
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Matches 47; Conservative 1
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   linear
   Query Match
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US-08-468-275-5
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LOCATION:
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, LOCATION:
US-09-007-466-3
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  US-09-007-466-3
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2 cuguuuccgaaauceguegueguegueguegueguegueguegucueaacuccaugeaaceug
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Sequence 5, Application US/09007466

Patent No. 6313092

GENERAL INFORMATION:
APPLICANT: HOLLADAY LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
CONTANDO.
  Query Match

49.7%; Score 46.2; DB 3; Length 141;
Best Local Similarity 51.6%; Pred. No. 4.8e-05;
Matches 47; Conservative 16; Mismatches 28; Indels
   PRIOR PAPLICATION DATA:

APPLICATION NUMBER: US 08/468,275

FILING DATE: 06-4UN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MILLER, D. BYRON

REGISTRATION NUMBER: 30,661

REFERENCEY/DOKET NUMBER: 30,661

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 496-8150

TELEPAC: (415) 496-8148

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ZIP: 94303-0802

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIFICATION: 530
   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-952-980B-5
   US-08-142-551B-8
  엄
  ò
  ò
  2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG 61
  26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAAACTCCCTCGAGGGTG 85
   0; Gaps
  Sequence 5, Application US/08952980B
| Sequence 5, Application US/08952980B
| Patent No. 633189
| GENERAL INFORMATION:
| APPLICANT: HOLLADAY, LESLIE A. APPLICANT:
| APPLICANT: OLDENBURG, KEVIN R. INCREASING THE
| TITLE OF INVENTION: BLECTROTRANSPORT FLUX OF POLYPEPTIDES
| TITLE OF INVENTION: BLECTROTRANSPORT FLUX OF POLYPEPTIDES
| NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: | ADDRESSES: AD
  Ouery Match

49.7%; Score 46.2; DB 3; Length 141;
Best Local Similarity 51.6%; Pred. No. 4.88-05;
Matches 47; Conservative 16; Mismatches 28; Indels (
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDERAURG, METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PRGE MILL ROAD
CITY: PALO ALTO
STATE: CALLFORNIA
  COUNTRY: PALO ALIVO
STATE: PALO ALIVO
COUNTRY: OBA
ZIP: 94303-0802
ZIP: 94303-0802
ZIP: 94303-0802
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: IBN PC Compatible
SOFTWARE
SAFETICATION NUMBER: US 0, 661
REPERENCE/DOCKET NUMBER: 2349 CIP 1
REPERENCE/DOCKET NUMBER: 2349 CIP 1
RELEFAX: (650) 496-8150
TELEFAX: (650) 496-8150
INFORMATION POR SEG ID NO: 3
SEQUENCE CHARRACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
   ::|||:|||:|||:|||:|||:||||:|||||:
86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
  MOLECULE TYPE: DNA (genomic) FEATURE:
   NAME/KEY: mat_peptide
LOCATION: 25
  NAME/KEY: CDS
LOCATION: 7..138
  RESULT 8
US-08-952-980B-5/c
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US-08-952-980B-3
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   Sequence 8, Application US/08142551B
; Sequence 8, Application US/08142551B
; Patent No. 5814603
; GENERALI INFORMATION:
; APPLICANT: Oldeburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: DOMEONES:
; COMPRESSPONDENCE ADDRESS:
; ADDRESSEE: Burne, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
   Query Match 49.7%; Score 46.2; DB 3; Length 141; Best Local Similarity 51.6%; Pred. No. 4.8e-05; Matches 47; Conservative 16; Mismatches 28; Indels
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ZIP: 22313
ZIP: 22313
ZIP: 25213
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
   56 TTGAATGGCTGCGTAAAAACTGCAGGACGT 26
CLASSIFTATION: 3.9.

ATTORNEY/AGENT INFORMATION:
NAME: MILLER D. BYRON

REGISTRATION NUMBER: 330,661

REFERENCE/DOCKET NUMBER: 2349 CIP 1

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10

TELEPAX: (650) 496-8150

TELEPAX: (650) 496-8150

TELEPAX: (650) 496-8150

INFORMATION FOR SEQ 10 NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH 141 base pairs

TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
   CLASSIFICATION: 43.5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-UNL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UNL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
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LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   linear
   DESCRIPTION:
DESCRIPTION:
   MOLECULE TYPE:
  US-09-068-738A-9
   US-09-068-738A-9
   CITY: 1
STATE:
   ઠે
  유
   ð
  /note= "Encodes amino acid sequence having six histamines that serves as a tag for the purification of the protein on a nickel column."
  2 CUGUIUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGGAACCUCAUGGAACGUG 61
  /note= "Encodes the leader peptide sequence that serves to direct the protein into inclusion bodies."
  49.7%; Score 46.2; DB 2; Length 207;
51.6%; Pred. No. 5.3e-05;
tive 16; Mismatches 28; Indels
  /note= "Encodes the protein or
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
  peptide of interest"
  000324-010
   Sequence 5, Application US/09463282D Patent No. 6500647
  ATJUMENT AND INCOMPANT OF A STANDEDNESS OF A STRANDEDNESS OF A STRANDED A S
  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
  FEATURE:
NAME/KEY: misc feature
LOCATION: 70..174
OTHER INFORMATION: pepti
  PEATURE:
NAME/KES:
COCATION: 175. 207
OTHER INFORMATION: /note:
OTHER INFORMATION: havin;
COTHER INFORMATION: purif.
FILING DATE: 22-OCT-1992 ATTORNEY/AGENT INFORMATION:
   NAME/KEY: misc feature LOCATION: 1..51 OTHER INFORMATION: /not
   47; Conservative
  TYPE: DNA
CORGANISM: Homo sapiens
US-09-463-282D-5
  OTHER INFORMATION: OTHER INFORMATION:
   LOCATION: 1..201
   Best Local Similarity
Matches 47; Conserv
   NAME/KEY: CDS
   US-09-463-282D-5
  Query Match
   LENGTH:
   g
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  US-10-340-484-14

US-20-10-340-484-14

Sequence 14, Application US/10340484

Sequence 14, Application US/10340484

GENERAL INFORMATION:
TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501

FILE REFERENCE: 2003-501

CURRENT APPLICATION UNMBER: US/10/340,484

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: 60/347,215
   Gaps
  Gaps
   Parent No. 6136564
GENERAL INFORMATION:
APPLICANT: KOPETZKI, Erhard
APPLICANT: KOPETZKI, Erhard
TITLE OF INVENTION: STREPTAVIDIN FUSION PROTEINS
TITLE OF INVENTION: STREPTAVIDIN FUSION PROTEINS
CORRESPONDENCE: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARENT FOX KINTNER PLOTKIN & KAHN
STREET: 1050 CONNECTICUT AVENUE, NW, SUITE 600
CITY: Washington
   ö
   .
Length 45;
  1 CATGGAACGTGTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 43
   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUT TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Pacentin Release #1.0, Version #1.30
SOFTWARE: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,738A
PTILING DATE: UNRORNA:
PTILING DATE: 11-NOV-1996
PRICATION NUMBER: PCT/EP 96/04850
FILING DATE: 11-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
NAME: Berman, Richard J.
NAME: Berman, Richard J.
NAME: Berman, Richard J.
NAME: REGISTRATION NUMBER: 39,107
REGISTRATION NUMBER: PLOBER: P
Query Match
46.7%; Score 43.4; DB 3;
Best Local Similarity 73.3%; Pred. No. 0.00027;
Matches 33; Conservative 11; Mismatches 1;
   Query Match 46.2%; Score 43; DB 3; I Best Local Similarity 76.7%; Pred. No. 0.00039; Matches 33; Conservative 10; Mismatches 0;
   other nucleic acid
/desc = "synthetic
oligonucleotide"
  Sequence 9, Application US/09068738A
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Gaps

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24 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 74
  0
   Ouery Match
42.8%; Score 39.8; DB 2; Length 234;
Best Local Similarity 64.7%; Pred. No. 0.0049;
Matches 33; Conservative 11; Mismatches 7; Indels (
   Query Match 42.8%; Score 39.8; DB 2; Length 234; Best Local Similarity 64.7%; Pred. No. 0.0049; Matches 33; Conservative 11; Mismatches 7; Indels
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US-08-733-446-61

Sequence 61, Application US/08733446

Patent No. 5856138

GENERAL INFORMATION:

TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: PRODUCTION THEREOF

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSE:

ADDRESSE: 130 Water Street
  COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PACHOLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 18-0CT-1996
CLASSIFTCATION NUMBER: US/08/733,446
FILING DATE: 18-0CT-1996
CLASSIFTCATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE: US/08/410N: US/08/4025
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 25.3.400
   LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
   LOCATION: 4,6
IDENTIFICATION METHOD: E
   TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
;
US-08-733-446-19
   CITY: Boston
STATE: Massachusetts
COUNTRY: US
  LOCATION: 1..234
NAME/KEY: mutation
LOCATION: 4,6
  US-08-733-446-61
  ò
  ò
  g
   ;
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   Gaps
  RESULT 13
US-08-733-446-19
is Sequence 19, Application US/08733446
is Sequence 19, Application US/08733446
is Betent No. 5556138
is GENERAL INFORMATION:
is APPLICANT: FUNDA, TSUNGHIKO
it TITLE OF INVENTION: HUMAN PRADATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: PRODUCTION THEREOF
is NUMBER OF SEQUENCES:
is ADDRESSES:
is ADDRESSES: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSES:
is ADDRESSES: CUSHMAN
street:
in 130 Water Street
   ;
0
   Ouery Match

42.8%; Score 39.8; DB 3; Length 102;
Best Local Similarity 64.7%; Pred. No. 0.0041;
Matches 33; Conservative 11; Mismatches 7; Indels
   COUNTRY:

US 21P:
US 2
   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid, synthetic DNA
   APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEBENOR: (617)523-3400
TELEEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
                PRIOR FILING DATE: 2002-01-10
PRIOR PRING DATE: 2002-01-01
PRIOR PILING DATE: 2002-01
PRIOR PELING DATE: 2002-01
PRIOR PELING DATE: 2002-01
PRIOR PELING DATE: 2002-02-8
PRIOR FILING DATE: 2002-03-8
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR APPLICATION NUMBER: 50/379,125
PRIOR SEQ IL DATE: 2002-05-08
NUMBER OF EQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
LENGTH: 102
   TYPE: DNA
CORGANISM: Homo sapiens
US-10-340-484-14
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US-08-733-446-20

1 Sequence 20, Application US/08733446

Patent No. 5856138

GENERAL INFORMATION:

TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS ENDURESS:

CORRESPENDENCE ADDRESS:

ADDRESSEE: USAID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: USAID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: USAID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & COUNTY: US DOSTON

STATE: Massachusetts
COUNTY: B. O2109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATION
SOFTWARE: PATENTIN NATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: WROMATION:
APPLICATION NUMBER: US/08/7926,787
APPLICATION NUMBER: US/08/7926,787
APPLICATION NUMBER: A2664
REGERENCE/DOCKET NUMBER: A2025
TELEFAX: (617)523-640
   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
FEATURE:
  ; NAME/KEY: CDS
; LOCATION: 1..237
; IDENTIFICATION METHOD:
US-08-733-446-20
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42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92 

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Search completed: November 24, 2005, 01:34:15 Job time: 74.6667 secs

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November 23, 2005, 23:59:22 ; Search time 412.667 Seconds (without alignments) 1863.616 Million cell updates/sec
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GenCore version 5.1.6
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  using sw model
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  DB
  Length
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  Query
Match
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Perfect score:
   Scoring table:
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   Sequence:
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  Database
  Run on:
   Result
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APPLICANT: Walker, Kenneth
APPLICANT: Walker, Kenneth
APPLICANT: Xiong, Fei
TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Seru
FILE REFERENCE: A-813A
CURRENT APPLICATION NUMBER: US/10/407,078
CURRENT PILING DATE: 2003-04-03
PRIOR FILING DATE: 2002-04-04

; Sequence 14, Application US/10407078; Publication No. US20030195154A1; GENERAL INFORMATION:

RESULT 2 US-10-407-078-14

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62 uugaauggcugcguaaaaaacugcaggacguu 93 

| RESULT 1  US-10-117-109-14  Sequence 14, Application US/10117109  Sequence 14, Application WS/10117109  Sequence 14, Application W. US20030191056A1  GENERAL INFORMATION:  APPLICANT: Walker, Kenneth  APPLICANT: Walker, Kenneth  APPLICANT: Walker, Kenneth  TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the  TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the  CURRENT PRILING DATE: 2002-04-04  NUMBER OF SEQ ID NOS: 42  SEQ ID NO 14  LENGTH: 489  TYPE: DNA  GORGANISM: Homo sapiens  US-10-117-109-14 | 38.2 41.1 102 9 US-10-775-204-1435 sequence 1435, | 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, 38.2 41.1 102 9 US-10-775-204-72 Sequence 69, 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434 Sequence 1434 | 38.2 41.1 102 9 US-10-775-204-57 Sequence 57, 38.2 41.1 102 9 US-10-775-204-60 Sequence 61, 38.2 41.1 102 9 US-10-775-204-61 Sequence 61,                                                             | 38.2 41.1 102 9 US-10-775-204-51 Sequence 51, 38.2 41.1 102 9 US-10-775-204-52 Sequence 52, Sequ | 38.2 41.1 102 9 US-10-775-204-24 Sequence 24.3 88.2 41.1 102 9 US-10-775-204-25 Sequence 25.                                                                                                                                                                                                                                                                                                                                                                                                                            | 38.4 41.3 874 6 US-10-437-038-7 Sequence 7, 38.4 41.3 874 6 US-10-359-091-7 Sequence 7,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 38.4 41.3 43.2 6 US-10-359-091-3 Sequence 3,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 38.4 41.3 348 6 US-10-359-091-1 Sequence 1, 38.4 41.3 432 6 US-10-437-038-3 Sequence 3,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 39 41.9 51 3 US-09-879-257A-52 Sequence 52,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 39 41.9 51 3 US-09-879-257A-51 Sequence 51,                                                                                                                                                                                                                                                                                                                                                                                         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41.1 102 9 US-10-775-204-64 Sequence 64 38.2 41.1 102 9 US-10-775-204-64 Sequence 64 38.2 41.1 102 9 US-10-775-204-78 Sequence 73 38.2 41.1 102 9 US-10-775-204-78 Sequence 74 38.2 41.1 102 9 US-10-775-204-78 Sequence 14: | 38.2 41.1 102 9 US-10-775-204-25 Sequence 23, 38.2 41.1 102 9 US-10-775-204-51 Sequence 5.2 38.2 41.1 102 9 US-10-775-204-51 Sequence 5.2 38.2 41.1 102 9 US-10-775-204-57 Sequence 5.2 38.2 41.1 102 9 US-10-775-204-60 Sequence 6.1 38.2 41.1 102 9 US-10-775-204-61 Sequence 6.1 38.2 41.1 102 9 US-10-775-204-64 Sequence 6.1 38.2 41.1 102 9 US-10-775-204-69 Sequence 6.1 38.2 41.1 102 9 US-10-775-204-72 Sequence 7.2 38.2 41.1 102 9 US-10-775-204-74 Sequence 7.2 38.2 41.1 102 9 US-10-775-204-73 Sequence 7.2 38.2 41.1 102 9 US-10-775-204-1434 Sequence 14.1 102 9 US-10-775-204-1435                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 38.2 41.1 102 9 US-10-775-204-51 Sequence 51.3 8.2 41.1 102 9 US-10-775-204-52 Sequence 52.3 8.2 41.1 102 9 US-10-775-204-57 Sequence 57.3 8.2 41.1 102 9 US-10-775-204-60 Sequence 67.3 8.2 41.1 102 9 US-10-775-204-61 Sequence 61.3 8.2 41.1 102 9 US-10-775-204-64 Sequence 61.3 8.2 41.1 102 9 US-10-775-204-69 Sequence 72.3 8.2 41.1 102 9 US-10-775-204-72 Sequence 72.3 8.2 41.1 102 9 US-10-775-204-1434 Sequence 14.3 8.3 8.2 41.1 102 9 US-10-775-204-1435 Sequence 14.3 8.3 8.3 8.3 8.3 8.3 8.3 8.3 8.3 8.3 8 | 38.2 41.1 102 9 US-10-775-204-51 Sequence 51. 38.2 41.1 102 9 US-10-775-204-52 Sequence 51. 38.2 41.1 102 9 US-10-775-204-67 Sequence 57. 38.2 41.1 102 9 US-10-775-204-60 Sequence 57. 38.2 41.1 102 9 US-10-775-204-61 Sequence 64. 38.2 41.1 102 9 US-10-775-204-64 Sequence 64. 38.2 41.1 102 9 US-10-775-204-69 Sequence 64. 38.2 41.1 102 9 US-10-775-204-74 Sequence 775-204-74 Sequence 775-204-74 Sequence 14. 38.2 41.1 102 9 US-10-775-204-1434 Sequence 14. 38.2 41.1 102 9 US-10-775-204-1434 Sequence 14. | 38.2 41.1 102 9 US-10-775-204-52 Sequence 52.3 41.1 102 9 US-10-775-204-52 Sequence 52.3 41.1 102 9 US-10-775-204-57 Sequence 57.3 41.1 102 9 US-10-775-204-60 Sequence 61.3 41.1 102 9 US-10-775-204-61 Sequence 61.3 41.1 102 9 US-10-775-204-64 Sequence 64.3 41.1 102 9 US-10-775-204-64 Sequence 64.3 41.1 102 9 US-10-775-204-72 Sequence 63.3 41.1 102 9 US-10-775-204-72 Sequence 14.3 41.1 102 9 US-10-775-204-1434 Sequence 14.3 58.2 41.1 102 9 US-10-775-204-1435 Sequence 14.3 59.2 41.1 102 9 US-10-775-204-1435 Sequence 14.3 59 | 38.2 41.1 102 9 US-10-775-204-52 Sequence 52. 38.2 41.1 102 9 US-10-775-204-57 Sequence 57. 38.2 41.1 102 9 US-10-775-204-60 Sequence 67. 38.2 41.1 102 9 US-10-775-204-61 Sequence 61. 38.2 41.1 102 9 US-10-775-204-64 Sequence 64. 38.2 41.1 102 9 US-10-775-204-69 Sequence 64. 38.2 41.1 102 9 US-10-775-204-69 Sequence 75. 38.2 41.1 102 9 US-10-775-204-1434 Sequence 14. | 38.2 41.1 102 9 US-10-775-204-57 Sequence 57, 38.2 41.1 102 9 US-10-775-204-60 Sequence 60, 38.2 41.1 102 9 US-10-775-204-61 Sequence 61, 38.2 41.1 102 9 US-10-775-204-64 Sequence 61, 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, 38.2 41.1 102 9 US-10-775-204-75 Sequence 72, 38.2 41.1 102 9 US-10-775-204-72 Sequence 1434 Sequence 1434 Sequence 1434 | 38.2     41.1     102     9     US-10-775-204-57     Sequence 57,       38.2     41.1     102     9     US-10-775-204-61     Sequence 60,       38.2     41.1     102     9     US-10-775-204-61     Sequence 61,       38.2     41.1     102     9     US-10-775-204-64     Sequence 64,       38.2     41.1     102     9     US-10-775-204-61     Sequence 69,       38.2     41.1     102     9     US-10-775-204-72     Sequence 72,       38.2     41.1     102     9     US-10-775-204-134     Sequence 1434       38.2     41.1     102     9     US-10-775-204-1434     Sequence 1435 | 38.2 41.1 102 9 US-10-775-204-60 Sequence 60, 38.2 41.1 102 9 US-10-775-204-64 Sequence 61, 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, 38.2 41.1 102 9 US-10-775-204-69 Sequence 64, 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434 | 38.2 41.1 102 9 US-10-775-204-60 Sequence 60, 38.2 41.1 102 9 US-10-775-204-61 Sequence 61, 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, 38.2 41.1 102 9 US-10-775-204-69 Sequence 69, 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, 38.2 41.1 102 9 US-10-775-204-13 Sequence 1434 Sequence 1435 | 38.2 41.1 102 9 US-10-775-204-61 Sequence 61, 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, 38.2 41.1 102 9 US-10-775-204-69 Sequence 64, 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434 Sequence 1435 | 38.2 41.1 102 9 US-10-775-204-61 Sequence 61, Ap 38.2 41.1 102 9 US-10-775-204-64 Sequence 69, Ap 38.2 41.1 102 9 US-10-775-204-69 Sequence 69, Ap 38.2 41.1 102 9 US-10-775-204-1434 Sequence 72, Ap 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, April 102 9 US-10-775-204-69 Sequence 64, April 102 9 US-10-775-204-12 Sequence 72, April 102 9 US-10-775-204-134 Sequence 1434, Sequence 1435, 41.1 102 9 US-10-775-204-1434 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-64 Sequence 64, Ap 38.2 41.1 102 9 US-10-775-204-69 Sequence 69, Ap 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-69 Sequence 69, Ap. 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, Ap. 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-69 Sequence by Ap 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, Ag 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-72 Sequence 72, Ap 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-1434 Sequence 1434, 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 38.2 41.1 102 9 US-10-775-204-1435 Sequence 1435, | 7.00                                              |                                                   | SHIVANIOT IX   |

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Sequence 33, Application US/10997700

Publication No. US20050239172A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Wal, U.
APPLICANT: Als, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA CONStructs for High Yield Production of Polypeptic TILE REPRENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US 60/393,710
CURRENT FILING DATE: 2004-11-24
PRIOR FILING DATE: 2002-05-24
PRIOR FILING DATE: 2002-05-24
PRIOR FILING PAPLICATION NUMBER: US 60/393,212
PRIOR FILING DATE: 2002-05-24
SEQ ID NOS: 93
SOFTWARE: PRESEQ for Windows Version 4.0
LENGTH. 10.0
LENGTH. 10.0
   Sequence 61, Application US/10997078
| Publication No. US20050221444A1
| GENERAL INFORMATION:
| APPLICANT: Wagner, F. APPLICANT: Xia, U. APPLICANT: Holmquist, B. APPLICANT: Restoragen, Inc. APPLICANT: Restoragen, Inc. | APPLICANT: Post | APPLICAN
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   2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61
   |:|::| ||||:|
2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAAACTCTATGGAACGTG 61
  2 cueuvucceaaauceeveeveeveeveeveeveeveeveeveeveareveraaceveeaaceve 61
  2 cueutucceaaaucesuseuseuseuseuseuseuseuseuseusaacuccauseaaceus 61
  Gaps
  ö
  Query Match 54.2%; Score 50.4; DB 9; Length 102; Best Local Similarity 52.2%; Pred. No. 6.2e-07; Matches 48; Conservative 18; Mismatches 26; Indels
  Query Match 54.2%; Score 50.4; DB 9; Length 102; Best Local Similarity 52.2%; Pred. No. 6.2e-07; Matches 48; Conservative 18; Mismatches 26; Indels (
   62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
  62 uugaauggcugcguaaaaacugcaggacguu 93
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
    NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 102
  ; OTHER INFORMATION: PTH(1-34).
US-10-997-078-60
   ), OTHER INFORMATION: PTH(1-34).
US-10-997-700-33
  TYPE: DNA
ORGANISM: Unknown
   TYPE: DNA
ORGANISM: Unknown
FEATURE:
   RESULT 5
US-10-997-700-33
  US-10-997-078-61
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  APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: A. U.
APPLICANT: A. U.
APPLICANT: Holmquist, B.
APPLICANT: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.010051
CURRENT APPLICANTON: WUMBER: US/10/997,078
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR PELLING DATE: 2003-05-23
PRIOR PELLING DATE: 2003-05-24
PRIOR FILING DATE: 2003-05-24
  US-10-407-078-43
US-10-407-078-43
Sequence 43, Application US/10407078
Publication No. US20030195154A1
GENERAL INFORMATION:
APPLICANT: Walker, Kenneth
APPLICANT: Xiong, Fei
TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Seru;
FILLE REFERENCE: A-813A
CURRENT APPLICATION NUMBER: US/10/407,078
CURRENT APPLICATION NUMBER: A-813
FRIOR APPLICATION NUMBER: A-813
FRIOR PILING DATE: 2003-04-03
FRIOR PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 75
SSOFTARE: Patentin version 3.1
LEGITH: 489
  61
  61
   64
  2 cuguuuccaaaaucaguaguaguaguaguaguaguaguagucugaacuccaugaacgug
  2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
   Gaps
  ;
0
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  Length 489;
  Length 489;
  Query Match 55.9%; Score 52; DB 6; Length 489 Best Local Similarity 51.1%; Pred. No. 2.6e-07; Matches 47; Conservative 20; Mismatches 25; Indels
  Query Match 55.9%; Score 52; DB 6; Length 489
Best Local Similarity 51.1%; Pred. No. 2.6e-07;
Matches 47; Conservative 20; Mismatches 25; Indels
   TGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   RESULT 4
US-10-997-078-60
'Sequence 60, Application US/10997078
'Publication No. US20050221444A1
'GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 75
; SOTTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 489
; TYPE: DNA
; ORGANIEN: Homo sapiens
US-10-407-078-14
  TYPE: DNA
CRGANISM: Homo sapiens
US-10-407-078-43
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TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic CURRENT PLICATION NUMBER: US/10/997,078

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: PCT/US03/16643

PRIOR APPLICATION NUMBER: DCT/US03/16643

PRIOR APPLICATION NUMBER: US 60/383,370

PRIOR PILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 148

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 141

LENGTH: 117
  APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Wagner, I.
APPLICANT: Peng, L.
APPLICANT: Peng, L.
APPLICANT: Rationagen, Inc.
TITLE OF INVENTION: Weethods and DNA Constructs for High Yield Production of Polypeptil
FILE REFERENCE: 1627.010/US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
FRIOR APPLICATION NUMBER: US/10/31/16643
FRIOR FILING DATE: 2003-05-23
FRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 252
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  2 cuentruccesasavicaeuceuceuceuceuceuceuceuceuceuceuceuceaceuc
  1:1:::| |||||:|
2 CTGTTTCTGAAATCCAGGTGACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
   |:|::| ||||:| |:|||||:|
2 CIGITITCIGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
  2 cuenturccanancesussussussussussussussussussussanceus
   Gaps
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   ..
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   Query Match

54.2%; Score 50.4; DB 9; Length 252;
Best Local Similarity 52.2%; Pred. No. 7.6e-07;
Matches 48; Conservative 18; Mismatches 26; Indelb (
   Length 117;
   Indels
   Query Match 54.2%; Score 50.4; DB 9; 1 Best Local Similarity 52.2%; Pred. No. 6.4e-07; Matches 48; Conservative 18; Mismatches 26;
  UNGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   ) OTHER INFORMATION: A synthetic PTH sequence. US-10-997-078-141
   ; Sequence 62, Application US/10997078; Publication No. US20050221444A1; GENERAL INFORMATION:
  TYPE: DNA
ORGANISM: Artificial Sequence
  ) OTHER INFORMATION: PTH(1-84).
US-10-997-078-62
Peng, L.
Xia, U.
Holmquist, B.
   ORGANISM: Unknown
  US-10-997-078-62
   TYPE: DNA
   FEATURE:
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  Sequence 34, Application US/10997700
; Sequence 34, Application VG20050239172A1
; Sequence 34, Application No. US20050239172A1
; Debilication No. US20050239172A1
; APPLICANT: Wagner, F.
; APPLICANT: Wagner, F.
; APPLICANT: Yia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti; PILE REPERBUE: 1627.0099081
; CURRENT APPLICATION NUMBER: US/10/997,700
; CURRENT FILING DATE: 2004-11-24
; PRIOR PPLING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTHER FESTESEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 111
   ö
  2 cuguruccananceduceuceuceuceuceuceuceuceuceucenceuceancuceanceuce 61
   |:|:::| |||||:| | CTGTTTCTGAAATCCAGGCTGAACCTGGGTAAACACCTGAACTTGGAACGTG 61
  61
  61
   2 cuguuccananceguegueguegueguegueguegueguegueguccaugaaccuc
   Gaps
   ö
   ;
0
  Length 111;
   54.2%; Score 50.4; DB 9; Length 111; 52.2%; Pred. No. 6.3e-07;
   26; Indels
   26; Indels
  54.2%; Score 50.4; DB 9; 52.2%; Pred. No. 6.3e-07; tive 18; Mismatches 26;
  ::|||:|||:|||:
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
   18; Mismatches
  CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2005-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 111
  Sequence 141, Application US/10997078; Publication No. US2005021444A1; GENERAL INFORMATION: APPLICANT: Wagner, F.
  ) OTHER INFORMATION: PTH(1-37).
US-10-997-078-61
   ) OTHER INFORMATION: PTH(1-37)
US-10-997-700-34
  Query Match
Best Local Similarity 52.27
Best Local Similarity 52.27
Conservative
  Query Match
Best Local Similarity 52.2.
Best Local Similarity 52.2.
  ORGANISM: Unknown
   ORGANISM: Unknown
  US-10-997-078-141
  TYPE: DNA
   TYPE: DNA
   FEATURE:
   FEATURE:
   RESULT 8
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, OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric protein. US-10-997-822-3
   ; OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic protein US-10-997-762-18
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54.2%; Score 50.4; DB 9; Length 276;
Best Local Similarity 52.2%; Pred. No. 7.8e-07;
Matches 48; Conservative 18; Mismatches 26; Indels (
   RESULT 13

US-10-997-82-3

i Sequence 3, Application US/10997822

publication No. US20050227314A1

i GENERAL INFORMATION:

APPLICANT: HOLMQTIST, B.

APPLICANT: Gensalk, X.

APPLICANT: Gensalk, X.

TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS

FILE REPRENCE: 1627.011US1

CURRENT APPLICATION NUMBER: US/10/997,822

CURRENT APPLICATION NUMBER: US/10/997,822

CURRENT PILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: US 60/383,484

PRIOR APPLICATION NUMBER: US 60/383,484

PRIOR APPLICATION NUMBER: US 60/383,484

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 276
  Sequence 18, Application US/10997762

Publication No. US20050227313A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APLICANT: Seo, Jin Seog
APPLICANT: SErydom, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REFERENCE: 1627.026US1
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2005-05-23
PRIOR FILING DATE: 2005-05-24
NUMBER OF SEO ID NOS: 23
SOFTWARE: PSEC FOR Mindows Version 4.0
  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                 62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  65 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 96
  TYPE: DNA ORGANISM: Artificial Sequence
  TYPE: DNA
ORGANISM: Artificial Sequence
   g
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                    à
  RESULT 10
US-10-997-700-35

Sequence 35, Application US/10997700

Publication No. US2055239172A1

GENERAL INFORMATION:

APPLICANT: Wagner, P.

APPLICANT: Xia, U.

APPLICANT: AIS, U.

APPLICANT: AIS, U.

APPLICANT: NUMBER: US/10/997,700

CURRENT APPLICATION NUMBER: US/10/997,700

CURRENT PILING DATE: 2004-11-24

PRIOR PILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: PASEEQ for Windows Version 4.0

LENGTH: 252
  Sequence 89, Application US/10997700

Publication No. US20050239172A1

GENERAL INFORMATION:

APPLICANT: Wagner, F.

APPLICANT: Weing, L.

APPLICANT: Weing, L.

APPLICANT: Holmquist, B.

TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti;

TITLE OF INVENTION: NUMBER: US/10/997,700

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: US 60/383,212

PRIOR APPLICATION NUMBER: US 60/383,212

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 264
   2 cueuvucceaaauceguegueguegueguegueguegueguegucueaacuccauegaacegue 61
   2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG 61
   0; Gaps
  Query Match

54.2%; Score 50.4; DB 9; Length 252;
Best Local Similarity 52.2%; Pred. No. 7.6e.70;
Matches 48; Conservative 18; Mismatches 26; Indels (
  Query Match 54.2%; Score 50.4; DB 9; Length 264; Best Local Similarity 52.2%; Pred. No. 7.7e-07; Matches 48; Conservative 18; Mismatches 26; Indels
   ; OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84). US-10-997-700-89
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62 TIGAAIGGCIGCGIAAAAAACIGCAGGACGIT 93
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  ), OTHER INFORMATION: PTH(1-84).
US-10-997-700-35
  TYPE: DNA
ORGANISM: Unknown
  RESULT 11
US-10-997-700-89
  FEATURE:
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Search completed: November 24, 2005, 04:46:56 Job time : 412.667 secs
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  Sequence 133, Application US/10997078

Sequence 133, Application US/10997078

Septicant No. US2005221444A1

GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti;
FILE REFERENCE: 125.70.0108.1

CURRENT APPLICATION NUMBER: US/10/997,078

CURRENT FILING DATE: 2004-11-24

PRIOR PILIOR DATE: 2003-05-23

PRIOR FILING DATE: 2003-05-23

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 148

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 133
   APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Tai, U.
APPLICANT: Tai, U.
APPLICANT: Applicant sid, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.009931, 2000.
CURRENT APPLICATION NUMBER: US/10/997, 700
CURRENT FILING DATE: 2004-11-24
PRIOR PILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 276
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  ö
  61
  2 CUGUIUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG 61
  2 CUGUIUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG
  0; Gaps
   Gaps
   .
0
  54.2%; Score 50.4; DB 9; Length 276; 52.2%; Pred. No. 7.8e-07; tive 18; Mismatches 26; Indels
Query Match 54.2%; Score 50.4; DB 9; Length 276; Best Local Similarity 52.2%; Pred. No. 7.8e-07; Matches 48; Conservative 18; Mismatches 26; Indels
   233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
   OTHER INFORMATION: A synthetic PCR product
   RESULT 14
US-10-997-700-75
Sequence 75, Application US/10997700
Publication No. US20050239172A1
GENERAL INFORMATION:
  TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
   Best Local Similarity 52.2%
Matches 48; Conservative
  US-10-997-078-133
  US-10-997-700-75
   Query Match
  FEATURE:
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; TYPE: DNA PATIFICIAL Sequence ; PEATURE: . ORGANISM: Artificial Sequence ; PEATURE: ; OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette. US-10-997-078-133
   ö
  2 CUGUIUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGUCAACUCCAUGGAACGUG 61
  Gaps
   .
0
   Length 282;
  Query Match

54.2%; Score 50.4; DB 9; Length 2

Best Local Similarity 52.2%; Pred. No. 7.8e-07;

Matches 48; Conservative 18; Mismatches 26; Indels
  227 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 258
   62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

November 24, 2005, 01:30:39; Search time 195 Seconds

(without alignments)

70.875 Million cell updates/sec

Perfect score: 93
Sequence: 1 gcuguuuccgaaaucggugg......guaaaaaacugcaggacguu 93
Scoring table: DENTITY NUC
Gapext 1.0
Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Database : Published\_Applications\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pubpna/US10 NEW\_PUB.seq:\*
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
6: /cgn2\_6/ptodata/1/pubpna/US1\_NEW\_PUB.seq:\*
7: /cgn2\_6/ptodata/1/pubpna/US1\_NEW\_PUB.seq:\*
8: /cgn2\_6/ptodata/1/pubpna/US1\_NEW\_PUB.seq:\*
9: /cgn2\_6/ptodata/1/pubpna/US1\_NEW\_PUB.seq:\*
10: /cgn2\_6/ptodata/1/pubpna/US1\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| ion                 | 11                | e 1, Appli      | m               | e 839, App        | e 35, Appl        | e 4301, Ap         |                   | 119,              | 100,               | 255,              | 775,              | 4, A            | 53                 | e 4, Appli      |                   | 82, 7             | 758,              | 374,              | 17, 1            | 19,               | e 33, Appl        | 34,               | e 621, App        |
|---------------------|-------------------|-----------------|-----------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-----------------|--------------------|-----------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|
| Description         | Sequence          | Sequence        | Sequence        | Seguence          | Sequence          | Sequence           | Sequence          | Seguence          | Sequence           | Sequence          | Seguence          | Sequence        | Sequence           | Sequence        | Sequence          | Sequence          | Sequence          | Sequence          | Sequence         | Sequence          | Sequence          | Sequence          | Sequence          |
| ΩI                  | US-10-927-641-116 | US-10-509-422-1 | US-10-509-422-3 | US-10-821-234-839 | US-10-131-826A-35 | US-10-793-626-4301 | US-10-821-234-766 | US-10-821-234-119 | US-10-467-962B-100 | US-10-821-234-255 | US-10-821-234-775 | US-10-526-731-4 | US-10-131-826A-531 | US-10-485-517-4 | US-10-821-234-268 | US-10-467-962B-82 | US-10-821-234-758 | US-10-802-796-374 | US-11-074-176-77 | US-11-015-546A-19 | US-10-994-820A-33 | US-11-013-247A-34 | US-10-793-626-621 |
| DB                  | 1                 | -               | Н               | ٦                 | П                 | 7                  | ч                 | -                 | -                  | Н                 | Н                 | Н               | Н                  | Н               | Н                 | ~                 | Н                 | ٦                 | 7                | 7                 | -                 | 7                 | н                 |
| Length DB           | 947               | 3507            | 3704            | 6497              | 3371              | 2536               | 1065              | 2218              | 2043               | 3893              | 963               | 2748            | 1150               | 2690            | 14770             | 477               | 7008              | 445               | 1152             | 1849              | 1956              | 2292              | 582               |
| %<br>Query<br>Match | 30.3              | 30.3            | 30.3            | 30.1              | 28.4              | 27.1               | 26.9              | 26.5              | 26.2               | 26.2              | 26.0              | 25.8            | 25.6               | 25.6            | 25.6              | 25.2              | 25.2              | 24.7              | 24.7             | 24.7              | 24.7              | 24.7              | 24.5              |
| Score               | 28.2              | 28.2            | 28.2            | 28                | 26.4              | 25.2               | 25                | 24.6              | 24.4               | 24.4              | 24.2              | 24              | 23.8               | 23.8            | 23.8              | 23.4              | 23.4              | 23                | 23               | 23                | 23                | 23                | 22.8              |
| ult<br>No.          | -                 | 0               | m               | 4                 | 2                 | ø                  | 7                 | 8                 | σ                  | 10                | 11                | 12              | 13                 | 14              | 15                | 16                | 11                | 18                | 19               | 20                | 21                | 22                | 23                |
| Result<br>No.       | υ                 | υ               | υ               |                   | U                 | υ                  | U                 | U                 | υ                  | υ                 |                   |                 |                    |                 | U                 |                   | υ                 | υ                 |                  | O                 | υ                 | U                 |                   |

| App               | App               | Appl             | Appl             | , Ap               | , Ap               | Appl             | App               | App               | App               | App               | 9, Appli        | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 353,              | 185,              | 35,              | 33,              | 4106,              | 4133,              | 19,              | 21,              | 23,              | 25,              | 27,              | 29,              | 31,              | 33,              | 35,              | 37,              | 47,              | 110,              | 100,              | 101,              | 108,              | ۰,<br>و         |
| Sequence          | Sequence          | Sequence         | Sequence         | Sequence           | Sequence           | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence          | Sequence          | Sequence          | Sequence          | Sequence        |
| US-11-074-176-353 | US-11-074-176-185 | US-11-082-389-35 | US-11-082-389-33 | US-10-793-626-4106 | US-10-793-626-4133 | US-11-065-943-19 | US-11-065-943-21 | US-11-065-943-23 | US-11-065-943-25 | US-11-065-943-27 | US-11-065-943-29 | US-11-065-943-31 | US-11-065-943-33 | US-11-065-943-35 | US-11-065-943-37 | US-10-821-234-47 | US-10-839-799-110 | US-10-839-799-100 | US-10-839-799-101 | US-10-839-799-108 | US-10-971-560-9 |
| 7                 | 7                 | Φ                | σ                | -                  | 7                  | 7                | 7                | 7                | 7                | 7                | 7                | ۲                | 7                | 7                | 7                | H                | ч                 | ٦                 | _                 | ч                 | -               |
| 1209              | 1224              | 1675             | 1758             | 3769               | 4249               | 1688             | 1688             | 1688             | 1688             | 1688             | 1688             | 1688             | 1688             | 1688             | 1688             | 8424             | 45                | 84                | 84                | 822               | 1506            |
| 24.5              | 24.5              | 24.5             | 24.5             | 24.5               | 24.5               | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 24.1             | 23.9              | 23.9              | 23.9              | 23.9              | 23.9            |
| 22.8              | 22.8              | 22.8             | 22.8             | 22.8               | 22.8               | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.4             | 22.2              | 22.2              | 22.2              | 22.2              | 22.2            |
| 24                | 25                | 26               | 27               | 28                 | 29                 | 30               | 31               | 32               | 33               | 34               | 35               | 36               | 37               | 38               | 39               | 40               | 41                | 42                | 43                | 44                | 45              |
|                   |                   | U                | υ                | υ                  | υ                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  | υ                |                   |                   | υ                 |                   | υ               |
|                   |                   |                  |                  |                    |                    |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                   |                   |                   |                   |                 |

## ALIGNMENTS

```
RESULT 1

Sequence 116, Application US/10927641

Sequence 116, Application US/10927641

Publication No. US20050244968A1

SEQUENCE 116, Application CO. US20050244968A1

SEMENRAL INFORMATION:
APPLICANT: Baglaton, Clare
APPLICANT: Baglaton, Clare
APPLICANT: Baglaton, Clare
APPLICANT: Lablam, Annette
APPLICANT: Lablam, Annette
APPLICANT: Lablam, Modification of Gene Expression
FILE REFRENCE: 11000.10364

TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: WUMBER: 12004-08-27

CURRENT FILING DATE: 2004-08-27

PRIOR PELICATION WUMBER: PRIOR APPLICATION WUMBER: US. No. 09/724,624

PRIOR APPLICATION WUMBER: US. No. 09/724,624

PRIOR APPLICATION WUMBER: US. No. 09/529401

PRIOR APPLICATION WUMBER: US. No. 09/529401

PRIOR APPLICATION WUMBER: US. No. 09/529401

PRIOR PLING DATE: 2000-02-24

PRIOR APPLICATION WUMBER: US. No. 09/529401

PRIOR PLING DATE: 2000-02-24

PRIOR APPLICATION WUMBER: US. No. 09/726,599

PRIOR APPLICATION WUMBER: US. No. 09/726,599

PRIOR PRIING DATE: 2000-02-24

PRIOR PRIING DATE: 2000-03-25

NUMBER OF SEQ ID NOS: 143

SOFTWARE: PRESENCE OF Windows Version 4.0

SEQ ID NO 116

SEQ ID NO 116

CURCANISM: Excalyptus grandis
US-10-27-641-116

QUETY MARCH
BASE LOCAL Similarity 56.1%; Pred. No. 1.7;

Base Local Similarity 56.1%; Pred. No. 1.7;

Base Local Similarity 61.1%; Pred.
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2 CUGUTUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGU 42 | |: || || || ||:||:||:||:||:||:||: 537 CAGTGCCCAATGGTGGTGGTGGTGGTGGTGGTGGT 497

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   30.3%; Score 28.2; DB 1; Length 3507; 60.6%; Pred. No. 2.1; ive 10; Mismatches 3; Indels 0;
  Query Match 30.3%; Score 28.2; DB 1; Length 3704; Best Local Similarity 60.6%; Pred. No. 2.2; Matches 20; Conservative 10; Mismatches 3; Indels 0;
   US-10-509-422-3/C
Sequence 3, Application US/10509422
Sequence 3, Application US/10509422
Sequence 3, Application US/10509422
PUBLICALION NO. US20050244825A1
GENERAL INFORMATION:
TITLE OF INFORMATION: Human BMP2 Inducible Kinases
TITLE OF INFORMATION: Human BMP2 Inducible Kinases
CURRENT PEPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-03-30
PRIOR FILING DATE: 2002-03-30
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: SEQ ID NOS: SEQ ID NOS: SEQ ID NOS: SEQ ID NO 3
ENGRH: AND 310-4
Sequence 1, Application US/10509422

PUblication No. US2005024482541

GENERAL INCRMATION:

APPLICANT: Liou, Simon

TITLE OF INVENTION: Human BMP2 Inducible Kinases

FILE REFERENCE: 004974.01015

CURRENT APPLICATION NUMBER: US/10/509,422

CURRENT FILING DATE: 2004-09-24

PRIOR FILING DATE: 2003-03-27

PRIOR FILING DATE: 2003-03-27

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/406,936

PRIOR PILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/406,936

NUMBER OF SEQ. ID NOS: 9

NUMBER OF SEQ. ID NOS: 9
   ||| : ||:||:||:||:||:||:||:||:||:||:|
  10 GAAAUCGGUGGUGGUGGUGGUGGUGGUGGU 42
   10 GAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGU
  Query Match 30.3
Best Local Similarity 60.6
Matches 20; Conservative
  TYPE: DNA
; ORGANISM: Homo sapiens
US-10-509-422-1
  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-509-422-3
   SEQ ID NO 1
LENGTH: 3507
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RESULT 4
(S-10-821-234-839)
Sequence 839, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: LADAL, Ivan

g

```
APPLICANT: WACAGUEDE, COLLIN A.
APPLICANT: WACAGUEDE, COLLIN A.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
FILE REFERENCE: P3330RIC128
CURRENT APPLICATION NUMBER: U5/10/131,826A
CURRENT FILING DATE: 1937-06-128
RIOR RPLILAGE TOWN NUMBER: 60/056974
PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056913
PRIOR PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
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   16 geugeugeugeugeugeugeugeugeuceuchaacuccaugeaaceuguaaaugecugeeu 75
APPLICANT: Stache-Crain, Birgit
APPLICANT: Addarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 82.A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILIG DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILICATION NUMBER: US 0/462,047
PRIOR PILICATION NUMBER: US 0/462,047
NUMBER: OF SEQ ID NOS: 1704
SOFTWARE: PL SEQ Genes Version 1.0
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   0
   Query Match 30.1%; Score 28; DB 1; Length 6497; Best Local Similarity 43.3%; Pred. No. 2.8; Matches 26; Conservative 14; Mismatches 20; Indels
   Sequence 35, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
  Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
   APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
   Godowski, Paul J. Gurney, Austin L.
   Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
  Sherwood, Steven
Smith, Victoria
   ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-821-234-839
   RESULT 5
US-10-131-826A-35/c
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Gaps

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264 GITTCCATGGCTGGTGGTGGGGTTGTGAGTGGCAGTCGTGGGTCGTGGTC 205
   4 GUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGUCUGAACUCCAUGGAACGUGUU 63
  Query Match 26.9%; Score 25; DB 1; Length 1065; Best Local Similarity 40.0%; Pred. No. 16; Matches 26; Conservative 14; Mismatches 25; Indels
; ORGANISM: Homo sapiens
US-10-821-234-766
  US-10-821-234-119
  NAME/KEY: CDS
   SEQ ID NO 100
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  Sequence 76, Application US/10821234

Sequence 76, Application US/205055114A1

GENERAL INFORMATION:

APPLICANT: Labat, Tran

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

TILLE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT PILING DATE: 2004-04-07

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt. SEQ_genes Version 1.0

SEQ ID NO 766

LENGTH: 1065
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   20 GUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAA 79
   RESULT 6
US-10-793-626-4301/c
US-10-793-626-4301/c
Sequence 4301, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFREENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-01-04
PRIOR PLILING DATE: 1999-11-09
PRIOR PLILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN UNC - 2.1
  15 coeuceuceuceuceuceuceuceuceuceuceuceaacuccauceaaceucuucaaugecuece
  Gaps
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550 SEQ ID NO 35.
   OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: nucleic acid sequence US-10-793-626-4301
  ö
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  Length 2536;
   28.4%; Score 26.4; DB 1; Length 3371; 46.7%; Pred. No. 7.6;
   27.1%; Score 25.2; DB 1; Length 2:
43.5%; Pred. No. 17;
tive 12; Mismatches 23; Indels
   21; Indels
  Query Match 28.4%; Score 26.4; Dr
Best Local Similarity 46.7%; Pred. No. 7.6;
Matches 28; Conservative 11; Mismatches
   TYPE: DNA ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity 43.5%
Matches 27; Conservative
   TYPE: DNA
ORGANISM: Homo Sapien
  1658 AA 1657
   80 AA 81
   US-10-821-234-766/c
   US-10-131-826A-35
  SEQ ID NO 4301
LENGTH: 2536
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   RESULT 8

US-10-821-234-119/c
; Sequence 119, Application US/10821234
; Publication No. US20050253114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Andarmani, Susan
; TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REPERENCE: 821A
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 119
  KESULI 3

VESTIO-467-962B-100/C

Sequence 100, Application US/10467962B

Publication No. US20050246784A1

GENERAL INFORMATION:

APPLICANT: Plesch, Gunnar

APPLICANT: Dleschner, Klaus

APPLICANT: Blau, Aetrid

APPLICANT: Mathieu

TITLE OF INVENTION: Identification of Herbicidally Active Substances

FILE REFERENCE: 200 857

CURRENT APPLICATION NUMBER: US/10/467,962B

CURRENT FILING DATE: 2003-08-14

PRIOR PILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 109

SOFTWARE: Patentin Vers. 2.0
   16 equequequequequequequequeuceadeaaccadeaaceucuneaaugec 70
   ö
   Query Match 26.5%; Score 24.6; DB 1; Length 2218; Best Local Similarity 47.3%; Pred. No. 25; Matches 26; Conservative 10; Mismatches 19; Indels 0
   LOCATION: (1)..(2043)
OTHER INFORMATION: ORF K5J14.11, Linie 229091
   TYPE: DNA ORGANISM: Arabidopsis thaliana
   TYPE: DNA
ORGANISM: Homo sapiens
   204 GCCTG 200
64 GAAUG 68
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US-10-467-962B-100

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5-10-131-826A-531
Sequence 531, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
RESULT 12
US-10-526-731-4
; Sequence 4, Application US/10526731
; Publication No. US20050244437A1
; GENERAL INFORMATION:
   Goddard, Audrey
Godowski, Paul J.
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
  APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
  ; TYPE: DNA; ORGANISM: Toxoplasma gondii
  Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
   SEQ ID NO 4
   q
  ò
  | Sequence 775, Application US/10821234 |
| Sequence 775, Application US/10821234 |
| Sequence 775, Application US/10821234 |
| Publication No. US20050255114A1 |
| GENERAL INFORMATION: |
| APPLICANT: Labat, Ivan |
| APPLICANT: Andarmani, Susan |
| APPLICANT: Andarmani, Susan |
| APPLICANT: Andarmani, Susan |
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia |
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia |
| TITLE REPERENCE: B21A |
| CURRENT FILING DATE: 2004-04-07 |
| PRIOR FILING DATE: 2004-04-07 |
| PRIOR FILING DATE: 2003-04-07 |
| NUMBER OF SEQ ID NOS: 1704 |
| SOFTWARE: PL_SEQ_genes Version 1.0 |
| SEQ ID NO 775 |
| LENGTH: 963 |
| LENG
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   APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
TITE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATE: 2004-04-07
CURRENT FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
LENTH: 3893
  Gaps
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   Query Match 26.2%; Score 24.4; DB 1; Length 3893; Best Local Similarity 61.5%; Pred. No. 32; Matches 16; Conservative 9; Mismatches 1; Indels 0.
           DB 1; Length 2043;
  DB 1; Length 963;
   8; Indels
  1; Indels
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  3 nemnecessas anced need encence of concerned 39
  / Match 26.0%; Score 24.2; D
Local Similarity 51.4%; Pred. No. 29;
Nes 19; Conservative 10; Mismatches
Query Match 26.2%; Score 24.4; E
Best Local Similarity 69.2%; Pred. No. 29;
Matches 18; Conservative 7; Mismatches
  2641 Grédrégrégrégrégrégrégre 2616
   17 GUGGUGGUGGUGGUGGUGGU 42
  12 AAUCGGUGGUGGUGGUGGUGGUG 37
   89 AAGCGGTGGTGGTGGTGGTG 64
  Sequence 255, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
  , ORGANISM: Homo sapiens
US-10-821-234-255
   ; ORGANISM: Homo sapiens
US-10-821-234-775
   RESULT 10
US-10-821-234-255/c
  RESULT 11
US-10-821-234-775
  DNA
  Query Match
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Matches
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APPLICANT: GGGGGAKE, PAUL J.
APPLICANT: GGGGGAKE, PAUL J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sterwood, Steven
APPLICANT: Sterwood, Steven
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Abang, Zemin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Abang, Zemin K
APPLICANT: Abang, Zemin K
APPLICANTON: ACIDE ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: 60/05931
PRIOR FILING DATE: 1997-09-17
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  38 guegucuesacuccauecaaceueuneaaueccueccuaaaaacuec 85
  Query Match 25.8%; Score 24; DB 1; Length 2748; Best Local Similarity 54.2%; Pred. No. 40; Matches 26; Conservative 7; Mismatches 15; Indels
APPLICATION AND NOBEL IN V.
TITLE OF INVENTION: live attenuated parasite vaccine FILE REFERENCE: 2002-017-EB.
CURRENT APPLICATION NUMBER: US/10/526,731
CURRENT FILING DATE: 2005-03-04
PRIOR PELING DATE: 2005-09-20
NUMBER OF SEQ ID NOS: 29
SOUTWARE: PATENTIN VERSION 3.2
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Search completed: November 24, 2005, 04:56:48 Job time: 195 secs
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  1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGGAACGU 60
  Sequence 268, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Arache-Crain, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FIRE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
   Gaps
  Gaps
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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   Length 5690;
   DB 1; Length 1150;
   Query Match 25.6%; Score 23.8; DB 1; Length 50 Best Local Similarity 35.8%; Pred. No. 53; Matches 24; Conservative 16; Mismatches 27; Indels
   Query Match 25.6%; Score 23.8; DB 1; Length 1 Best Local Similarity 51.2%; Pred. No. 39; Matches 22; Conservative 9; Mismatches 12; Indels
  16 equequequequequequequequequenceauceaac 58
  GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Softer, Simon
APPLICANT: Foster, Simon
APPLICANT: Mond, James
ITILE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: PIOGESSWO
CURRENT PELLING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
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PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2002-01-09
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  TYPE: DNA
ORGANISM: Staphylococcus aureus
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  ; ORGANISM: Homo Sapien
US-10-131-826A-531
   GTTGTAT 586
   GUUGAAU 67
  US-10-821-234-268/c
   LENGTH: 5690
   61
   TYPE: DNA
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Gaps
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  Query Match 25.6%; Score 23.8; DB 1; Length 14770; Best Local Similarity 59.3%; Pred. No. 64; Matches 16; Conservative 9; Mismatches 2; Indels 0;
   12126 GGTGGTGGTAGTGGTGGTAGTGGT 12100
   16 GGUGGUGGUGGUGGUGGUGGUGGU 42
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LENGTH: 14770
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; ORGANISM: Homo sapiens
US-10-821-234-268
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November 21, 2005, 16:17:24 ; Search time 186 Seconds (without alignments) 37.796 Million cell updates/sec
  2443163
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
   2443163 segs, 439378781 residues
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
   using sw model
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  A Geneseq 21:*

1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003s:*
9: geneseqp2003bs:*
9: geneseqp2003bs:*
   1 avseiglmhnlggggg 16
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
   - protein search,
  SEQ-NEW
  score:
   Scoring table:
   OM protein
   Database :
   Searched:
   Sequence:
  Title:
Perfect
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |            | Description | Human tet | Parathyro | Parathyro | [Gly13] -h | Parathyro | Mutant pe | [Ala1] -pa | Rat parat | Native ra | Amino aci | Novel hum | Rat parat | Parathyro | Rat parat | Rat parat | Human ami | Human par | Human par | Human par | Human par | Parathyro | PTH/PTHrP | Human par | PTH-rP fu |
|-----------|------------|-------------|-----------|-----------|-----------|------------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| SUMMARIES |            |             | Aay96988  | Aay96975  | Aay96973  | Aar58104   | Adz76826  | Abg76365  | Aab01861   | Aab96896  | Aab84776  | Adr14864  | Adu24382  | Adw88336  | Adz76832  | Abp71487  | Adw88343  | Aay98016  | Aay98049  | Aay98045  | Aay98048  | Aay98044  | Aau73060  | Adq75375  | Aay04203  | Aay96978  |
|           |            |             |           |           |           |            |           |           |            |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|           |            | ED.         | AAY96988  | AAY96975  | AAY96973  | AAR58104   | ADZ76826  | ABG76365  | AAB01861   | AAB96896  | AAB84776  | ADR14864  | ADU24382  | ADW88336  | ADZ76832  | ABP71487  | ADW88343  | AAY98016  | AAY98049  | AAY98045  | AAY98048  | AAY98044  | AAU73060  | ADQ75375  | AAY04203  | AAY96978  |
|           |            |             | -         | _         |           | 2<br>A     | •         |           | 3          | 4<br>A    | 4 A       |           | 8<br>A    | Ø         | -         | 9<br>9    | 4<br>6    |           |           | •         | Α<br>Ε    | _         |           | •         |           | Α.        |
|           |            | 8           |           |           |           |            |           |           |            | 4         | 4         | 4         | Δ.        | 4         | -         |           | -         |           | ۲,        |           | 80        |           |           |           |           | _         |
|           |            | Length      | 450       | 31        | Ε.        | 38         | 1         | 13        | 14         | 7,        | 1,        | 1,        | 1,        | 7         | ii        | 5         |           | 7         | 7         | 7         | 7         | ~         | ĕ         | ĕ         | 'n        | m         |
|           | *<br>Query | Match       | 85.5      | 83.1      | 74.7      | 74.7       | 71.1      | 71.1      | 71.1       | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      | 71.1      |
|           |            | Score       | 71        | 69        | 62        | 62         | 59        | 29        | 59         | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        | 59        |           | 59        |
|           | Result     | No.         | н         | 7         | e         | 4          | ហ         | 9         | 7          | 80        | σ         | 10        | 11        | 12        | 13        | 14        | 15        | 16        | 17        | 18        | 19        |           | 21        | 22        |           | 24        |

| 977074094971                                                                      | Aau73037 Native nu Aau73037 Native nu Aau73037 Native nu Aac7426 Rat matur Adc7425 Rat matur Adc7425 Rat matur Adc7425 Rat matur Adc7426 Parathyro Aar58226 N-alpha-m Aar5826 N-alpha-m Aar5826 N-alpha-m Aar5826 N-alpha-m Aar5826 (Alai]-hP Ada66231 Rat parat Ada7833 Parathyro Aar5826 (Alai]-hP Ade6633 Rat parat Ada7839 Parathyro Ada7839 Parathyro Ada7839 Parathyro Ada7839 Parathyro Ada7843 Rat parat Adx18518 Rat prH ( Adx16531 Rat parat Adx16818 Rat prH ( Adx16818 Rat parat Adx16818 Ra | 18 Human pa<br>17 Human pa |
|-----------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| AD12477 AAY9801 AAP8217 AAR0792 AAR0792 AAR0998 AAW1999 AAW2000 AAY980110 AAB9110 | AAB84777 AAB84777 AAB84777 ABP71499 ABP71499 AD074395 AD074395 AD074395 AD794476 AAR58248 AAR58248 AAR58262 AAR58262 AAR58262 AAR58262 AAR58219 AAR58219 AAR58219 AAR58211 AAP73623 AAP74470                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AAR888                     |
|                                                                                   | ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | - 80 80                    |
|                                                                                   | ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 67.                        |
|                                                                                   | 88888888888888888888888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 200                        |

seq-new.rag

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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-IO (preferably 4)); B is a C-terminal binding portion of PTH-134); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor eformation, bone mass, determining rates of bone reformation, bone resorption and/or bone remodaling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by
Aay98046 Human par
Aay98052 Human par
Aab81074 Human par
   New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   PTH; parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
  39. .450
/label= PTH-1_receptor
/note= "Human PTH-1 receptor residues 182-593"
  Location/Qualifiers
1. .23
/label= Signal sequence
/note= "Human PTH-1 receptor residues 1-23"
  Jueppner H;
   Human tethered PTH-1 receptor, Tether-Rll.
  ALIGNMENTS
  Gardella TJ, Kronenberg HM, Potts JT,
 AAY98046
AAY98052
AAB81074
  AAY96988 standard; protein; 450 AA
  24. .34
/label= PTH(1-11)
35. .38
/label= Linker
39. .450
  Example 4; Fig 19; 119pp; English.
   99WO-US031108.
   98US-0114577P.
 w w 4
  (first entry)
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
   WPI; 2000-452384/39.
N-PSDB; AAA51737.
67.5
67.5
67.5
   WO200039278-A2
  Homo sapiens.
Synthetic.
Chimeric.
  31-DEC-1998;
  31-OCT-2000
   06-JUL-2000
 56 56
  Peptide
  Peptide
  Peptide
   Protein
  RESULT 1
 98
99
100
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   Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R. are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH)? L is a linker molecule present n times (where n is a positive inceper 1-L0 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-PP) (1-34); R. I is the PTH-I receptor signal sequence; and R is (a portion of) PTH-I receptor signal sequence; and R is (a portion of) PTH-I receptor characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases
inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
  New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
   Gaps
   PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
   ö
   Parathyroid hormone functional domain conjugate peptide PG7
   Score 71; DB 3; Length 450;
Pred. No. 0.0085;
   1; Indels
   1. .9
/label= PTH N-terminal signaling_domain
/note= "residues 1-9"
  17. .31
/label= PTH C-terminal binding_portion
/note= "residues 17-31"
  Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
   0; Mismatches
   Location/Qualifiers
   AAY96975 standard; peptide; 31 AA.
  Claim 7; Page 93; 119pp; English.
  10. .16
/label= linker
   99WO-US031108.
  98US-0114577P.
   85.5%;
93.3%;
  31-OCT-2000 (first entry)
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Matches 14; Conservative
   (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
   WPI; 2000-452384/39.
N-PSDB; AAA51730.
   Sequence 450 AA;
  WO200039278-A2
  Homo sapiens.
Synthetic.
   30-DEC-1999;
  31-DEC-1998;
  06-JUL-2000.
  AAY96975;
  Key
Peptide
  Peptide
   Peptide
  RESULT 2
  AAY96975
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The new compounds are used for treating mammalian conditions

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   Compounds of the structure or formula S-(L) n-B, R-1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R-1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inn-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
  New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
  Gaps
   PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
  ö
   Parathyroid hormone functional domain conjugate peptide PG5
   83.1%; Score 69; DB 3; Length 31; 87.5%; Pred. No. 0.00085;
  2; Indels
  1. 9
| /abel= PTH N-terminal_signaling_domain
/note= "resīdues 1-9"
  15. 30
/label= PTH C-terminal binding portion
/note= "residues 15-31"
  Jueppner H;
  0; Mismatches
  Potts JT,
  Claim 7; Page 92-93; 119pp; English
   Location/Qualifiers
  AAY96973 standard; peptide; 31 AA.
  10. .14
/label= linker
   Gardella TJ, Kronenberg HM,
   98US-0114577P.
   1 AVSEIQLMHGGGGGGG 16
   1 AVSEIQLMHNLGGGGG 16
   (first entry)
  14; Conservative
   GARDELLA T J.
KRONENBERG H
   2000-452384/39.
  (JUEP/) JUEPPNER H.
  (GARD/) GARDELLA T
  Query Match
Best Local Similarity
   POTTS J T.
  N-PSDB; AAA51729
   Sequence 31 AA;
   WO200039278-A2
   30-DEC-1999;
   31-DEC-1998;
   31-OCT-2000
   sapiens
   06-JUL-2000
   Synthetic
   AAY96973;
   (KRON/)
  Peptide
   Peptide
   Peptide
  Ношо
   Matches
   RESULT
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sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
   This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
  Gaps
  Gaps
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  5
  New active para-thyroid hormone variants - used for treating preventing osteoporosis etc.
  Length 38;
  Length 31;
  0; Indels
  Indels
  ö
  74.7%; Score 62; DB 2;
92.3%; Pred. No. 0.014;
tive 1; Mismatches
  74.7%; Score 62; DB 3;
87.5%; Pred. No. 0.011;
   Rainer
   0; Mismatches
   Waelchli R,
  Example 101; Page 39; 92pp; English.
  AAR58104 standard; peptide; 38 AA
  92GB-00015009.
92GB-00026815.
92GB-00026859.
92GB-0001691.
93GB-0001692.
93GB-00007673.
  1 AVSEIQLMHNLGGGGG 16
  14
   93GB-00014384
  1 AVSEIQLMH--GGGGG
   Ouery Match
Best Local Similarity 8/..
Local 14; Conservative
  Conservative
   Schneider H,
  [G1y13] -hPTH(1-38) -OH
  WPI; 1994-018352/03.
  (SANO ) SANDOZ LTD.
  Best Local Similarity
Matches 12; Conserv
   hypoparathyroidism
  Ä
  Sequence 31 AA;
  12-JUL-1993;
   20-SEP-1994
   15-JUL-1992
  19-APR-1993
   3B2269176-A
  23-DEC-1992
23-DEC-1992
  28-JAN-1993
  02-FEB-1994
   28-JAN-1993
  4-APR-1993
   Synthetic.
  Lewis I,
  Query Match
  RESULT 4
  AAR58104
   88888888888888888
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4

```
Producing antibodies to a three-dimensional epitope of a bioactive human parathyroid hormone for diagnosing or treating e.g., hyperparathyroidism by immunizing an animal with the hormone and recovering the antibodies.
  The present invention relates to a method for producing antibodies to a three-dimensional epitope of bioactive human parathyroid hormone (hPTH). The method comprises immunising an animal with the bioactive hPTH and recovering antibodies from the animal. The antibodies specifically recognise the three-dimensional structure of the bioactive hPTH. The method is useful for manufacturing a medicament for diagnosing or treating hyperparathyroidism or hypoparathyroidism. ABG76344-ABG76370 represent mutants or "variants" of peptide sequences from hPTH
Human, three-dimensional epitope; human parathyroid hormone; hPTH; bioactive hPTH; antibody production; hyperparathyroidism; antithyroid; hypoparathyroidism; immunostimulant; mutant; mutein.
   Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP; calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.
  71.1%; Score 59; DB 6; Length 13; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
   [Ala1]-parathyroid hormone peptide(1-14), SEQ ID NO:5.
   (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.
   /note= "C-terminal amide"
  Location/Qualifiers
  Disclosure; Page 10; 69pp; English.
   AAB01861 standard; peptide; 14 AA.
   03-JUL-2002; 2002WO-US021356.
  99WO-US024481
   03-JUL-2001; 2001US-00898398.
  (first entry)
   Query Match
Best Local Similarity 100.
The 12; Conservative
   1 AVSEIQLMHNLG 12
  AVSEIQLMHNLG 12
   WPI; 2003-229379/22.
   WO2003003986-A2.
   Sequence 13 AA;
   WO200023594-A1
   Key
Modified-site
   Homo sapiens.
Synthetic.
   20-OCT-1999;
  Hutchison JS;
  11-SEP-2000
  Homo sapiens
Synthetic.
  27-APR-2000
  16-JAN-2003
   AAB01861;
  RESULT 7
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   The present invention relates to a method of producing an antibody to the N-terminal portrion of (1-84) parathyroid hormone (PTH) which comprises administering N-terminal peptide antigens corresponding to amino acid residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions of the invention are useful in determining bioactive intact PTH levels in serum, plasma and/or cell culture media and antibodies possessing a high degree of species cross-reactivity. The present equence is a parathyroid hormone (PTH) (1-12) antigenic N-terminal peptide. This N-terminal peptide sequence is obtained from mouse and rat species.
   Producing antibodies to the N-terminal portion of (1-84) parathyroid hormone (PTH) by administering a first peptide antigen to a host animal, useful in determining bioactive intact PTH levels in serum, plasma and/or cell culture media.
   Gaps
  Parathyroid hormone (PTH) (1-12) antigenic peptide, SEQ ID NO: 5.
   Mutant peptide #2 derived from human parathyroid hormone (hPTH).
   ö
  71.1%; Score 59; DB 9; Length 12;
100.0%; Pred. No. 0.012;
tive 0; Mismatches 0; Indels
  Claim 1; SEQ ID NO 5; 13pp; English.
  Parathormone; PTH; hormone; antigen
  Ā.
  ADZ76826 standard; peptide; 12 AA.
   ABG76365 standard; peptide; 13
  05-DEC-2000; 2000US-00730174.
   29-NOV-2004; 2004US-00998927.
   Zahradnik RJ, Lavigne JR;
   (first entry)
   (first entry)
          13
  1 SVSEIQLMHNLGG 13
  Local Similarity 100.
  1 AVSEIQLMHNLG 12
          1 AVSEIQLMHNLGG
  (ZAHR/) ZAHRADNIK R J. (LAVI/) LAVIGNE J R.
  WPI; 2005-344980/35.
  US2005095236-A1.
  Sequence 12 AA;
  Mus musculus.
Rattus sp.
  19-MAY-2003
   14-JUL-2005
   05-MAY-2005
   ADZ76826;
   Query Match
  Best Loc
Matches
  REBULT 5
AD76826
AD776826
AD776826
AD776826
AD7776
AD7777
AD7776

  ABG76365
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Gaps

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hypercalcaemia; anaemia; bone disease; renal impairment; ulcer; myopathy;
   AAB84776
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  The invention relates to a novel parathyroid hormone (PTH) peptide
(AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860.), and
biologically active derivatives thereof (AAB01858, AAB01861.)

Biologically active derivatives thereof (AAB01858, AAB01861.)

CO B01869). The peptides of the invention are at least 85% identical to the generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-Gly-LyA-X6 (AAB01857) where is a ser or Ala; X2 is He or Ly9; X3 is

CO CONSISTING ABOUNDES TRAGMEND OF EAST, The peptides of the invention also encompass fragments of peptides of the invention and on encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and so encompass fragments of peptides of the invention and to the recently identified PTH-2 receptor. PTH has a potent anabolic of effect on the skeleten, and mediates calcium reabsorption, enhances phosphate clearance and vitamin D synthesis in the kidney, A homologous consistency and mediates calcium reabsorption, enhances phosphate clearance and vitamin D synthesis in the kidney. A homologous conflicton are aither agonists of PTH, and also bind to the PTH-1 creeptor. They do not bind to the PTH-2 receptor antagonists (AAB01867-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-B01866) or are PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor antagonists are useful for reaction of the PTH-2 receptor antagonists are useful for reacting or are pTH-1/PTH-2 receptor antagonists are useful for reacting or and/or bone remodelling in a patient. The peptides of the invention are
   ö
   Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
   Gaps
  Rat; human; parathyroid hormone derivative; calcium homeostasis;
   ö
   Length 14;
  0; Indels
  Jueppner H;
   Score 59; DB 3;
Pred. No. 0.014;
   Mismatches
  Sardella TJ, Kronenberg HM, Potts JT,
  AAB96896 standard; peptide; 14 AA.
   ö
  Claim 3; Page 47; 73pp; English
   Rat parathyroid hormone(1-14).
   71.1%; {
100.0%;
   PTH-1/PTH-2 receptor agonists
                 98US-0105530P
  (first entry)
   Conservative
  1 AVSEIQLMHNLG 12
  AVSEIQLMHNLG 12
   GARDELLA T J.
KRONENBERG H M.
POTTS J T.
JUEPPNER H.
  WPI; 2000-339693/29.
  Local Similarity
ses 12; Conserv
  Sequence 14 AA;
                   22-OCT-1998;
  13-JUL-2001
  AAB96896
   Query Match
   (KRON/)
(POTT/)
  (GARD/)
   (JUEP/)
   Matches
   RESULT 8
  AAB96896
     셤
   2X2X5X8X8
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  The present invention provides a number of parathyroid hormone derivatives based on the rat and human hormone sequences. These peptides can be used in the treatment of human skeletal conditions, including osteoporosis, fractures and cartilage disorders, disruption of calcium homeostasis, which may cause severe bone disease, anaemia, renal impairment, ulcers, myopathy and neuropathy, hypercalcaemia and hyperparathyroidism. The present peptide was used in the exemplification
  Osteopathic; calcium homeostasis regulator; parathyroid hormome; PTH;
   Gaps
   Novel amino acid encoding polypeptides useful in the treatment of
   ö
   DB 4; Length 14;
0.014;
  0; Indels
neuropathy; hyperparathyroidism; osteoporosis; fracture cartilage disorder.
  Potts JT, Juppner H;
  Native rat parathyroid hormone peptide fragment #1.
  Jueppner
   0; Mismatches
  Potts JT,
   71.1%; Score 59; 100.0%; Pred. No.
   Example 2; Page 64; 100pp; English
   AAB84776 standard; peptide; 14 AA.
   Gardella TJ, Kronenberg HM,
  Gardella TJ, Kronenberg HM,
  29-SEP-2000; 2000WO-US026818
   29-SEP-1999; 99US-0156927P.
25-FEB-2000; 2000US-0185060P.
  25-FEB-2000; 2000WO-US004716.
  99US-0156927P
  25-JUL-2001 (first entry)
  (GEHO ) GEN HOSPITAL CORP.
  GEHO ) GEN HOSPITAL CORP.
   Best Local Similarity 100.
Matches 12; Conservative
   1 AVSEIQLMHNLG 12
  bone mass; osteoporosis.
   WPI; 2001-343161/36.
   the invention
   Sequence 14 AA;
   WO200123521-A2.
   WO200123427-A1.
  29-SEP-1999;
  osteoporosis.
   05-APR-2001.
   05-APR-2001
  Rattus sp.
  Rattus sp
   AAB84776;
  Query Match
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RESULT 11
  ADU24382
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   Treating mammalian conditions characterized by a decrease in bone mass e.g. old age or post-menopausal osteoporosis by administering to a subject a biologically active peptide or its analogs, fragments, salts or N- or C- derivatives.
   The present invention relates to parathyroid hormome (PTH) polypeptide derivatives, and the present sequence is one such derivative. PTH is a major regulator of calcium homeostasis. The PTH polypeptide derivatives are useful for treating conditions characterised by decreases in bone mass, such as old age esteoporosis and post-menopausal osteoporosis. The polypeptides are also useful for determining rates of bone reformation, bone resorption and/or bone remodaling, by administering the polypeptide into the bone, and effective bone mass-increasing amount to the peptide into the bone, by providing to the patient DNA encoding the peptide and expressing the peptide in vivo. The levels of GAMP and inositol phosphate can also be increased in a mammalian cell having PTH-1 receptors, by contacting the cell with a sufficient amount of the polypeptide.
                     New Parathyroid hormone (PTH) derivatives useful for treating conditions characterized by decreases in bone mass.
  Gaps
   bone mass; parathyroid hormone; PTH; lactam bridge; agonist;
PTH-1 receptor; old age; post-menopausal osteoporosis; osteoporosis.
  .
0
  Match 71.1%; Score 59; DB 4; Length 14; Local Similarity 100.0%; Pred. No. 0.014; Decal Similarity 0; Indels es 12; Conservative 0; Mismatches 0; Indels
   Amino acid sequence of a parathyroid hormone fragment.
   /note= "amidated residue"
  Disclosure; SEQ ID NO 37; 63pp; English
   Potts JT;
   Location/Qualifiers
   ADR14864 standard; peptide; 14 AA.
   Example 2; Page 67; 97pp; English.
   Gardella TJ, Kronenberg HM,
   24-JAN-2003; 2003WO-US002155.
  24-JAN-2003; 2003WO-US002155
   04-NOV-2004 (first entry)
  1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
  (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
  WPI; 2004-580854/56.
WPI; 2001-374252/39
  WO2004067021-A1
  Sequence 14 AA;
  Key
Modified-site
  12-AUG-2004
   Rattus sp.
  Query Match
Best Local S
Matches 12
   ADR14864;
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  This invention relates to a novel biologically active peptide (conformationally constrained parathyroid hormone analogues and derivatives of those homologues). The invention may be useful for the development of compounds with an endocrine-Gen, antithyroid, cardiovascular-Gen, CNS-Gen, gastrointestinal-Gen or osteopathic activity
  biologically active peptide; parathyroid hormone analogue; endocrine-Gen; antithyroid; cardiovascular-Gen; CNS-Gen; gastrointestinal-Gen; osteopathic; cAMP agonist; bone calcification promoter; parathyroid hormone-1 receptor agonist; calcium antagonist; bone mass; bone reformation; bone resorption; bone resorption; bone recoporasis; osteopenia; bone fracture; cartilage disorder; OTH-1 receptor; human.
The specification describes a method for treating mammalian conditions characterized by a decrease in bone mass. The method comprises administering to a subject a biologically active peptide of a formula given in the specification. The peptide is a parathyroid hormone (PTH) derivative containing amino acid substitutions at selected positions in the polypeptide as well as derivatives containing lactam bridges between receiptor. The method is useful in treating mammalian conditions characterized by a decrease in bone mass e.g. old age or post-menopausal osteoporosis. The present sequence represents a native rat PTH fragment.
  cells
  New conformationally constrained parathyroid hormone analogs and derivatives of those homologs, useful for raising cAMP levels in cells and treating conditions such as hyperparathyroidism and hypercalcemia.
  Gaps
  .
0
  Novel human parathyroid hormone-derived active peptide SeqID17.
   Carter P;
   11.1%; Score 59; DB 8; Length 14; larity 100.0%; Pred. No. 0.014; Conservative 0; Mismatches 0; Indels
   Potts JT, Kronenberg HM, Shimizu N,
   /note= "C-terminal amide"
  Disclosure; SEQ ID NO 17; 88pp; English.
   Location/Qualifiers
   ADU24382 standard; peptide; 14 AA.
   (GEHO ) GEN HOSPITAL CORP.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
  19-MAR-2003; 2003WO-US008261.
  19-MAR-2003; 2003WO-US008261.
   27-JAN-2005 (first entry)
  1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
   WPI; 2004-795421/78.
   Best Local Similarity
Matches 12; Conser
   Sequence 14 AA;
  WO2004093902-A1
   Key
Modified-site
   Gardella TJ,
   Homo sapiens.
Synthetic.
  04-NOV-2004.
   ADU24382;
   Query Match
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  The invention provides novel antagonists of the juxtaposition (J) domain of the parathyroid hormone (PTH or parathormone) receptor. These antagonists contain amino acid substitutions at selected positions in truncated PTH and PTH-related polypeptide and function by selectively binding the J domain of the receptor. The J domain is the region of the receptor (PTR) that spans the seven transmembrane domain and the extracellular loops. PTH polypeptide antagonists of the invention can be used to treat conditions relating to PH/PTR hyperactivity, such as hypercalcemia including malignant hypercalcemia (claimed), primary hyperparathyroidism, and Jansen's chondrodysplasia. They can also be used to identify other ligands (e.g. using a high-throughput screen) that bind to PIR, such as small molecule PTH minetic compounds, or for the pharmacological analysis of PIR ligands for their selectivity, e.g. for
acting as a cAMP agonist, bone calcification promoter, agonist of parathyroid hormone-1 receptor or calcium antagonist. The invention may be useful for treating mammalian conditions associated with decrease in bone mass or for determining rates of bone reformation, bone resorption and/or bone remodeling. The invention may also be useful for prophylaxis and/or brone remodeling. The invention may also be useful for prophylaxis cxample osteoporosis, osteopenia, fractures and cartilage disorders, and for treating a medical disorder that results from altered or excessive action of the OTH-1 receptor. The present sequence is that of a human parathyroid hormone-derived biologically active peptide of the invention.
  conformationally constrained parathyroid hormone analogs useful in treatment of e.g. hypercalcemia primary and hyperparathyroidism.
  Cardiovascular.gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.; antithyroid; parathormone; hypercalcemia; metabolic disorder.
   Gaps
   ;
0
   71.1%; Score 59; DB 8; Length 14; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
  /note= "C-terminal amide"
  Disclosure; SEQ ID NO 26; 49pp; English
  Location/Qualifiers
   ADW88336 standard; peptide; 14 AA.
   16-JUL-2004; 2004WO-US022830
   17-JUL-2003; 2003US-0487589P
   (GEHO ) GEN HOSPITAL CORP
  Local Similarity 100 nes 12; Conservative
  1 AVSEIQLMHNLG 12
  AVSEIQLMHNLG 12
  Rat parathyroid hormone
  WPI; 2005-132386/14.
  WO2005009358-A2
   Sequence 14 AA;
   Modified-site
  21-APR-2005
   03-FEB-2005.
  Gardella TJ
  Rattus sp
   Query Match
  ADW88336
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  The present invention relates to a method of producing an antibody to the N-terminal portion of (1-84) parathyroid hormone (PTH) which comprises administering N-terminal peptide antigens corresponding to amino acid residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions of the invention are useful in determining bioactive intact PTH levels in serum, plasma and/or cell culture media and antibodies possessing a high degree of species cross-reactivity. The present sequence is a parathyroid hormone (PTH) (1-15) antigenic N-terminal peptide. This N-terminal peptide sequence is obtained from mouse and rat species.
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the J domain. The present sequence is that of rat PTH(1-14). PTH derivatives of the invention contain changes in sequence relative to this wild-type sequence. Note: this sequence is given as SEQ ID NO:26 in Figure 1 of the specification, but is different from the sequence given in SEQ ID NO:26 on page 16 ADW88342.
  Producing antibodies to the N-terminal portion of (1-84) parathyroid hormone (PTH) by administering a first peptide antigen to a host animal, useful in determining bioactive intact PTH levels in serum, plasma and/or
  Gaps
   Gaps
  Parathyroid hormone (PTH) (1-15) antigenic peptide, SEQ ID NO: 11.
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  DB 9; Lenson 0.015; 0; Indels
   Length 14;
   0; Indels
   DB 9; 1
   Mismatches
   71.1%; Score 59; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches
  Disclosure; SEQ ID NO 11; 13pp; English.
  71.1%; Score 59;
100.0%; Pred. No.
   Parathormone; PTH; hormone; antigen.
  ADZ76832 standard; peptide; 15 AA.
   .
0
   05-DEC-2000; 2000US-00730174.
   29-NOV-2004; 2004US-00998927
   я,
;
  (first entry)
  Local Similarity 100.
hes 12; Conservative
  Conservative
  1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
  12
   Lavigne
  AVSEIQLMHNLG
   1 AVSEIQLMHNLG
   ZAHRADNIK R
LAVIGNE J R.
   WPI; 2005-344980/35.
  Best Local Similarity
Matches 12; Conserv
  cell culture media.
   US2005095236-A1.
  Sequence 15 AA;
  Sequence 14 AA;
   Zahradnik RJ,
   Mus musculus.
  14-JUL-2005
   05-MAY-2005
   Rattus sp.
  Query Match
  ADZ76832;
  Query Match
   ZAHR/)
   (LAVI/)
  Best Loca
Matches
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The invention provides novel antagonists of the juxtaposition (J) domain of the parathyroid hormone (PTH or parathormone) receptor. These antagonists contain amino acid substitutions at selected positions in truncated PTH and PTH-related polypeptide and function by selectively cruncated PTH and PTH-related polypeptide and function by selectively creceptor (PIR) that spans the receptor. The J domain is the region of the extracellular loops. PIR polypeptide antagonists of the invention can be extracellular loops. PIR polypeptide antagonists of the invention can be creeptor (PIR) that spans the seven transmembrane domain and the cused to treat conditions relating to PHPIR Myperactivity, such as provided an antagonists of the invention can be considered to the second parameter of the property of the present sequence (C) pharmacological analysis of PIR ligands for their selectivity, e.g. for the J domain. The present sequence is that of rat PTH(1-21). PTH contains the sequence is that of rat PTH(1-21). PTH contains the sequence relative to this will be the specification, but is different from the sequence given in SEQ ID NO:27 on page of the invention contain changes in sequence given in SEQ ID NO:27 in Figure 1 ADW88337.
  Parathyroid hormone peptide; PTH; renal cell; osseous cell; human; signal transduction; osteoporosis; amino-terminal modification; bone disease; parathyroid hormone receptor; osteopania; hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
Cardiovascular-gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.; antithyroid; parathormone; hypercalcemia; metabolic disorder.
  New conformationally constrained parathyroid hormone analogs useful the treatment of e.g. hypercalcemia primary and hyperparathyroidism.
  Human amino-terminal modified parathyroid hormone analogue # 7.
  Query Match 71.1%; Score 59; DB 9; Length 21; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 12; Conservative 0; Mismatches 0; Indels
   Disclosure; SEQ ID NO 27; 49pp; English
   Location/Qualifiers
1
  AAY98016 standard; peptide; 27 AA.
   17-JUL-2003; 2003US-0487589P.
   16-JUL-2004; 2004WO-US022830.
  04-SEP-2000 (first entry)
  (GEHO ) GEN HOSPITAL CORP.
   1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
   WPI; 2005-132386/14.
  WO2005009358-A2
  Sequence 21 AA;
   Key
Modified-site
  Homo sapiens
  Gardella TJ;
   Rattus sp.
  RESULT 16
   AAY98011

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XXX AAY

XXX AAY

XXX B HU

XXX B Bay

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  The invention relates to conformationally constrained parathyzoid hormone (PTH) analogueues, in particular, derivatives of PTH (1-134), PTH (1-121), PTH (1-13), PTH (1-13), PTH (1-13), PTH (1-11), PTH (1-14), PTH (1-13), PTH (1-12), PTH (1-11), PTH (1-10) polypeptides. The PTH analogues are useful for treating mammalian conditions characterized by decrease in bone mass (e.g. old age osteoporosis, post-menopausal osteoporosis) or by the need for bone sprowth for e.g. in treating fractures or cartilage disorders and for raising cyclic adenosine monophosphate (CAMP) levels in cells. They are also useful for treating osteopenia. The PTH peptide analogues can also be used as diagnostic probes, as antigens to prepare antibodies for use as diagnostic probes and as molecular weight markers. The present sequence represents a rat native PTH peptide fragment.
   Conformationally constrained parathyroid hormone (PTH) analogs, useful for treating conditions characterized by decrease in bone mass (e.g. osteoporosis) or by the need for bone growth (e.g. in treating fractures or cartilage disorders).
  PTH; parathyroid hormone; anabolic; cAMP; bone mass; osteopenia; rat.
  Gaps
  ;
0
   Rat parathyroid hormone (PTH) peptide fragment (residues 1-21).
   71.1%; Score 59; DB 6; Length 21; 100.0%; Pred. No. 0.022; tive 0; Mismatches 0; Indels
  Disclosure, Page 114; 135pp; English.
  21 AA.
  ABP71487 standard; peptide; 21 AA.
   23-JUL-2001; 2001US-0306866P. 02-OCT-2001; 2001US-0326212P.
  19-JUL-2002; 2002WO-US022922.
  ADW88343 standard; peptide;
  21-APR-2005 (first entry)
  Local Similarity 100.
   1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
  Rat parathyroid hormone
  (GARD/) GARDELLA T J.
  WPI; 2003-268010/26.
  WO2003009804-A2.
  Sequence 21 AA;
  Gardella TJ;
   15-MAY-2003
   06-FEB-2003
  Rattus sp.
   ADW88343;
   ABP71487;
   Query Match
   Best Loc
Matches
  RESULT 15
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ADW88343
ID ADW8
XX
AC ADW8
XX
XX
DT 21-A
XX
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Gaps

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98US-0109938P.
   99WO-US027863
99WO-US027863
  (GEHO ) GEN HOSPITAL CORP.
  WPI; 2000-400076/34.
  osteopathic; PTH
  Sequence 27 AA;
  WO200031266-A1.
24-NOV-1999;
   25-NOV-1998;
                      25-NOV-1998;
  Homo sapiens
   24-NOV-1999;
   32-JUN-2000
  AAY98045;
   Query Match
  RESULT 18
  AAY98045
   ò
  유
  Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the mino terminal is important for signal transduction. The present sequence is a human PTH peptide, with an amino-terminal modification which results in effective activation of the PTH-2 receptor and therefore downstream cignalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma wellow a variety of cancers: breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oesophagus. This peptide would be suitable for prophylaxis and treatment of the above fracture repair. The present sequence would be suitable for fracture repair. The present sequence is modified to have a desamino
   .
0
   New parathyroid hormone (PTH) analogs having one or more amino acid substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful for treating old age osteoporosis and post-menopausal osteoporosis.
  Gaps
   Human; parathyroid hormone; signal transduction; osteoporosis; osteopaenia; hyporazathyroidism; fracture repart; hypercalicaemia; breast cancer; lung cancer; prostate cancer; multiple myeloma; hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
   ö
  Score 59, DB 3; Length 27;
Pred. No. 0.029;
0; Mismatches 0; Indels
  /note= "Ala is desamino residue"
   71.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
  Gardella TJ;
  Human parathyroid hormone peptide # 9.
  Disclosure; Page 64; 69pp; English.
   AAY98049 standard; peptide; 27 AA.
  99WO-US027656
  98US-0110152P
  (first entry)
  Bringhurst FR, Takasu H,
  Best Local Similarity 100.
Matches 12; Conservative
  1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
  (BRIN/) BRINGHURST F R. (TAKA/) TAKASU H.
   (TAKA/) TAKASU H.
(GARD/) GARDELLA T J.
  WPI; 2000-400045/34
  osteopathic; PTH
  Sequence 27 AA;
                         WO200031137-A1
   Ното варіепв.
  23-NOV-1999;
   25-NOV-1998;
  04-SEP-2000
   02-JUN-2000.
   02-JUN-2000
  AAY98049;
   Query Match
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Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal of PTH is important for signal transduction. Various PTH peptides were produces with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders obseoporosis, osteopaenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and epidermoid cancers of the head, neck and oesophagus. The myeloma and epidermoid cancers of the head, neck and oesophagus. The present sequence is a PTH peptide, with an Ala residue at position 19 and cancers of the head, neck and oesophagus. Consulting and ligand binding. PTH peptides with an Arg residue at calcust signalling and ligand binding. PTH peptides with an Arg residue at position of signalling and ligand binding. PTH peptides with an Arg residue at position of the above mentioned disorders and fracture repair.
  ö
  Gaps
  Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
  Human, parathyroid hormone, signal transduction, osteoporosis, osteopaenia, hypoparathyroidism, fracture repair, hypercalicaemia, breast cancer, lung cancer, prostate cancer, multiple myeloma, hypernephroma, head and neck epidermoid cancer, oesophagus cancer;
   ö
   71.1%; Score 59; DB 3; Length 27; 100.0%; Pred. No. 0.029; ive 0; Mismatches 0; Indel8
   Potts JT;
   Gardella TJ,
  Human parathyroid hormone peptide # 5.
  Disclosure; Page 69; 75pp; English.
   AAY98045 standard; peptide; 27 AA.
98US-0109938P
   04-SEP-2000 (first entry)
   Bringhurst FR, Takasu H,
  GEHO ) GEN HOSPITAL CORP
   Best Local Similarity 100.
Matches 12; Conservative
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  1 AVSEIQLMHNLG 12
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Claim 8; Page 69; 75pp; English.

Potts JT;

Gardella TJ,

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Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
   Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
  Human parathyroid hormone peptide # 8.
   Disclosure; Page 68; 75pp; English.
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   98US-0109938P
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  (GEHO ) GEN HOSPITAL CORP.
Takasu H,
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  WPI; 2000-400076/34.
             WPI; 2000-400076/34.
   Sequence 27 AA;
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Bringhurst FR,
   24-NOV-1999;
   25-NOV-1998;
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  02-JUN-2000.
   AAY98048;
  Query Match
   Best Loca
Matches
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Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the cabboxyl terminal of PTH is important for pTH receptor binding, while the amino terminal is important for gignal transduction. Various PTH peptides were produces with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream cignalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteoposis, os
  Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. Various PTH peptides
  Gaps
  Human; parathyroid hormone; signal transduction; osteoporosis; osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia; breast cancer; lung cancer; prostate cancer; multiple myeloma; hypernephroma; head and neck epidermoid cancer; oesophagus cancer; osteopathic; PTH.
  Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
  ö
  71.1%; Score 59; DB 3; Length 28; 100.0%; Pred. No. 0.03; ive 0; Mismatches 0; Indels
  Gardella TJ, Potts JT;
  Human parathyroid hormone peptide # 4.
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   Claim 6; Page 68; 75pp; English.
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  (GEHO ) GEN HOSPITAL CORP.
   Bringhurst FR, Takasu H,
   04-SEP-2000 (first entry)
  Local Similarity 100.
nes 12; Conservative
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   1 AVSEIQLMHNLG 12
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   25-NOV-1998;
  02-JUN-2000.
  AAY98044;
   Query Match
Best Local S
   Matches
  RESULT 20
  AAY9804
а
   8
  calls initiating signal transduction. It has been identified that the carboxyl terminal of PTH) binds to PTH receptors in renal and osseous calbs, initiating signal transduction. It has been identified that the carboxyl terminal is important for signal transduction. Various PTH peptides were produces with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopaenia, hypoparathycoidism and momber of hypoparathycoidism and avariety of cancers: Dreast, lung and prostate carcinoma, multiple myeloms and epidermoid cancers of the head, neck and oesophagus. The present sequence is a PTH peptide, with an Ala residue at position 19. The Ala and Arg residues both improve downstream signalling via phospholipase C (PLC) and ligand binding. The creatment of the above mentioned disorders. In addition, the present readunce would be suitable for fracture repair
   ö
   Gaps
   Human; parathyroid hormone; signal transduction; osteoporosis; osteopania; hypoparathyroidism; fracture repair; hypercalcaemia; breast cancer; unitiple myeloma; hypernephroma; head and neck epidermoid cancer; oesophagus cancer; osteopathic; PTH.
   Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
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were produces with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteopensis, osteopenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers: breast, lung and prostate carcinoma, multiple present sequence is a PTH peptide, with an Ala residue at position 1 and an Arg residue at position 19. The Ala and Arg residues both improve downstream signalling via phospholipase C (PLC) and ligand binding. The present peptide may therefore be used as a PTH receptor agonist for the treatment of the above mentioned disorders. In addition, the present sequence would be suitable for fracture repair
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Sequence 28 AA;

Gaps ; 0 Query Match

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Best Local Similarity 100.0%; Pred. No. 0.03;
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ALIGNMENTS

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R;Vasicok, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
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R;Keutemann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.!
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-1
  AUSDIAL
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J. Biol. Chem. 259, 3120-3129, 1984
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R;Schmelzer, H.
Ay. Chane Technol. 21, 228-229, 1984
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à Op

AVSEIQLMHNLG 43

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Length 105; 0; Indels

Score 58; DB 2; Pred. No. 0.029; 1; Mismatches (

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22 AISEIQLMHNLG 33

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A,Cross-references: UNIRROT:P01268; UNIPARC:UPI0000132907; GB:K01938
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr., Proc. Natl. Acad. Sci. U.S.A, 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid horm!
A;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
  R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Pott Hoppe-Seyler's Z. Physiol. Chem. 311, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
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A; Note: the authors translated the codon GAA for residue 50 as Gly
R; Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.:
Proc. Natl. Acad. Sci. U. S.A. 71, 653-656, 1974
A; Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
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Gene 28, 319-329, 1982
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid A;Reference number: A24949; MUID:84262483; PMID:6086460
   R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
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R;Chu, L.L.H.; Huang, W.Y.; Littledike, B.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial aminc
  A; Kergear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J. R. Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J. R; Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J. Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A; Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum A; Reference number: A91660; MUID:75059220; PMID:4474131
A; Contents: annotation; synthesis of residues 32-65
A; Note: the biologically active amino-terminal 34 residues of parathyroid hormone were sat renal adenylate cyclase assay and with the bovine hormone's active region in the chic R; Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Helv. Chim. Acta 56, 470-473, 1973
A; Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A; Reference number: A91635; MUID:73227467; PMID:4721748
A; Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rate caused a distinct increase in plasma calcium level R; Hendy, G.N.; Kronenberg, H.M.; Potter, J. 1965-7369, 1981
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  counter to calcitonin
   A; Accession: A90390
   Query Match
   Local
   Matches
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Darathyroid hormone precursor - dog
parathyroid hormone precursor - dog
parathyroid hormone precursor - dog
parathyroid lupus familiaris (dog)
C.Species: Canis lupus familiaris (dog)
C.Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C.Accession: JC4202
C.Bate: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C.Accession: JC4202
A.Fiselor and C.C.
  lipid-transfer protein (sterol or nonspecific) - Methanobacterium thermoautotrophicum (stiplid-transfer protein (sterol or nonspecific) - Methanobacterium thermoautotrophicum (species: Methanobacterium thermoautotrophicum (space: Ob-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 (c) Accession: G68205 (c) Access
                  A,Accession: ISO411
A,Status: prelimitary; translated from GB/EMBL/DDBJ
A)Status: prelimitary; translated from GB/EMBL/DDBJ
A)ACCUST PROBLEMBA
A,Residues: 1-119 «KHO»
A,Cross-references: UNIPARC:UPI0000132909; GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g
C,Superfamily: parathyroid hormone; parathyroid hormone homology
F;1-25/Domain: signal sequence #status predicted «SIG»
F;2-31/Domain: propeptide #status predicted «PIH»
F;30-34/Domain: parathyroid hormone homology «PTH»
F;30-34/Domain: parathyroid hormone #status predicted «MAT»
  Gaps
  Gaps
  Gaps
  ö
  ö
  Score 47; DB 2; Length 383;
Pred. No. 6.9;
3; Mismatches 3; Indels
  63.9%; Score 53; DB 2; Length 119; 83.3%; Pred. No. 0.21; arive 2; Mismatches 0; Indels
  / Match
Local Similarity 83.3%; Pred. No. 0.29;
local Oloservative 1; Mismatches 1; Indels
  Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
  Query Match 63.9
Best Local Similarity 83.3
Matches 10; Conservative
  32 SVSEMQLMHNLG 43
  1 AVSEIQLMHNLG 12
  :||||| |||||
32 SVSEIQFMHNLG 43
  1 AVSEIQLMHNLG 12
  Query Match
Best Local S
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  qq
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Afitle: Bovine parathyroid hormone: amino acid sequence.

Afracessence number: A93773, MUID: 71063634; PMID: 5275384

Afracession: A93773

Afracession: A93773

Afracession: A93773

Afracession: A93773

Afracession: A93773

Afracession: A93774

Afracession: A93775

Afracession: A937
  A34937

A34937

A34937

A34937

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Species: O7-Sep-1990 #text_change 09-Jul-2004

C;Accession: A34937; 150411

R;Russell, J.; Sherwood, L.M.

Mol. Endocrinol. 3, 325-331, MUD: 89219100; PMID: 2710135

A;Reference number: A34937; MUD: 89219100; PMID: 2710135

A;Rolecule type: mRNA

A;Residues: 1-119 - RUSA

A;Rossidues: 1-119 - RUSA

A;Cross-references: UNIPPOT: D15743; UNIPARC: UP10000132909; GB: M31604; NID: 9212767; PIDN: R;Rosla, S; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.

J. Bone Miner: Res. 3, 689-689; 1988

A;Reference number: 150411; MUD: 89284968; PMID: 3251402
  ö
  Gaps
  ö
  Match
Local Similarity 91.7%; Pred. No. 0.096;
tes 11; Conservative 0; Mismatches 1; Indels
  1 AVSEIQLMHNLG 12
  AVSEIQFMHNLG 43
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Best Loc Matches

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A, Cross-references in UNIPACT: P05219; UNIPARC: UPI0000136A39; EMBL: AL031743; PIDN: CAA21099. J
A, Experimental source: strain 972h-; cosmid c26H8
R, Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
Mol. Biol. Cell 9, 1757-171, 1988
A, Title: Identification of novel temperature-sensitive lethal alleles in essential beta-f
A, Reference number: Z22579; MUID: 98324923; PMID: 9658169
A, Accession: T43623
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-448 «RAD>
A, Residues: 1-448 «RAD>
A, Residues: L448 «RAD>
A, Cross-references UNIPARC: UPI0000136A39; EMBL: AF042827; PIDN: AAC21454.1
A, Experimental source: strain 972
C, Genetics:
   A;Gross-references: UNIPROT:066668; UNIPARC:UPI00000F0F2B; GB:U20824; NID:g695172; PIDN::
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
  A;Residues: 1-395 «KEE»
A;Gross-references: UNIPARC:UPI000007A51C; EMBL:U29441; NID:g1322213; PIDN:AAC47210.1; Þ
A;Experimental source: ATCC 50330
   tubulin beta chain - Hexamita sp. (strain ATCC 50330) (fragment)
C;Species: Hexamita sp.
A;Variety: ATCC 50330
C;Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 07-Dec-1999
C;Accession: 570637
F;Keeling, P.J; Doolittle, W.F.
EMBO J. 15, 2285-2290, 1996
A;Title: A non-canonical genetic code in an early diverging eukaryotic lineage.
A;Reference number: 870634; MUID:96208514; PMID:8641293
  ö
  ö
  A; Status: preliminary; nucleic acid sequence not shown; translation not shown
  C.Species: equine herpesvirus 2
C.Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
   Gарв
   Gaps
  C;Accession: S5561
R;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
  ö
   ö
  55.4%; Score 46; DB 2; Length 456; 63.6%; Pred. No. 12; 2; Indel8;ive 2; Mismatches 2; Indel8
   Length 448;
   ..
2
  ; DB 2;
: 12;
preliminary; translated from GB/EMBL/DDBJ
  2; Mismatches
   hypothetical protein 66 - equine herpesvirus 2
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   A; Map position: 2
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Best Local Similarity 63...
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  EIFHRLGGGGG 18
   6 QLMHNLGGGGG 16
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  A; Molecule type: DNA
A; Residues: 1-456 <TEL>
   A; Molecule type: DNA
  A;Accession: S55661
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  C; Species: Schizosaccharomyces powder C; Species: Schizosaccharomyces powder C; Species: Schizosaccharomyces powder C; Accession: A21649
C; Accession: A21649
R; Hiraoka, Y; Toda, T; Yanagida, M.
Cell 39, 349-358, 1984
A; Title: The NDA3 gene of fission yeast encodes beta-tubulin: a cold-sensitive nda3 muta A; Reference number: A21649; MUID:85048945; PMID:6094012
A; Accession: A21649
A; Accession: A21649
A; Accession: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-448 < HIR>
A; Residues: 1-448 < HIR>
A; C; Superfamily: tubulin
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C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43624
R;Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
Mol. Biol. Cell 9, 1757-1771, 1998
A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-A;Reference number: Z22579; MUID:98324923; PMID:9658169
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A;Molecule type: DNA
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A;Cross-references: UNIPROF: PD5219; UNIPARC: UPI0000168807; EMBL: AF042828; PIDN: AAC21455.
A;Experimental source: strain 972
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   ö
   RESULT 11
140019
140019
beta tubulin - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40019; T43623
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
A;Reference number: Z21899
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  / Match 55.4%; Score 46; DB 2; Length 448; Local Similarity 56.2%; Pred. No. 12; Pred. 9; Conservative 2; Mismatches 5; Indels
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  tubulin beta chain - fission yeast (Schizosaccharomyces pombe)
   5; Indels
  ..
7
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  A;Map position: 2
A;Introns: 4/3; 21/2; 35/2; 53/3; 349/1
C;Superfamily: tubulin
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ALOGFOLTHSLGGGTG 144
  16
  1 AVSEIQLMHNLGGGGG 16
  :|| : ||:||
361 AEIGMTHNIGGTGG 374
   16
  1 AVSEIQLMHNLGGGGG
   Conservative
  Local Similarity
hes 9; Conserva
  A; Accession: T40019
  Query Match
   C, Genetics:
A, Gene: nda3
  Best Loc
Matches
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probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
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C;Accession: A84497
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h
M:; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.; h
M: Koo, M. S. Moffat, K.S.; Cronin, L.A.; Shen, M.I.; Town, C.D.; Fuser, U.S.; Cronin, L.A.; Shen, M.I.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Mixure 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84497
A;Accession: A84497
A;Accession: A84497
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A;Residues: 1-962 <GTTO>
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A;Genetics:
A;Gene
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84638
E;Lin, X.; Kaul, S.; Rounsley, S.D.; Shear, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.; h
M.; Koo, M.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-7768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
   tubulin beta chain - silkworm

Uspecies: Bombyx mori (silkworm)

C;Species: Bombyx mori (silkworm)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: 833177

R;Mita, K.

Submitted to the EMBL Data Library, September 1993

A;Reference number: 837177

A;Accession: 837177

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A;Accession: 837177

A;Accession: 87177

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A;Accession: 87177

A;Cross-references: UNIPROT:P41385; UNIPARC:UPI0000136A12; EMBL:X74951; NID:g402173; PIDB

C;Superfamily: tubulin
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Best Local Similarity 66.7%; Pred. No. 39;

Matches 8; Conservative 1; Mismatches 3; Indels
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656 VQLTHRLGGRGG 667
   5 IQLMHNLGGGGG 16
   ||:|:|||| |
134 QLVHSLGGGTG 144
   ||:|:||| |
134 QLIHSLGGGTG 144
   6 OLMHNLGGGGG 16
   6 QLMHNLGGGGG 16
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  A; Molecule type: DNA
A; Residues: 1-420 (MILE)
A; Residues: 1-420 (MILE)
A; Residues: 1-420 (MILE)
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A; Experimental source: clone F55C5
B; Harris, B
Submitted to the EMBL Data Library, August 1996
A; Reference number: 219896
A; Reference number: 219896
A; Retension Preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
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A; GGenetics
A; Genetics
A; Genetics
B; Miltrons: 56/1; 120/1; 224/1; 379/1
C; Superfamily: tubulin
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tubulin beta chain - chicken

c)Species: Gallus Gallus (chicken)

C)Species: Gallus gallus (chicken)

C)Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C)Accession: A27424 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C)Accession: A27424 #sequence and expression of the divergent beta-tubulin in chicken erythrocyt

A).Title: The sequence and expression of the divergent beta-tubulin in chicken erythrocyt

A).Reference number: A27424

A).Residues: 1-446 *AUR.

A).Residues: 1-446 *AUR.

A).Cossion: A27424

A).Cossio
A,Note: the sequence of residues 388-395 and the corresponding nucleic acid sequence are C,Genetics:
A,Genetic code: SGC5
C,Superfamily: tubulin
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0
  RESULT 14
12216
hypothetical protein T04H1.9 - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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Submitted to the EMBL Data Library, August 1996
A;Reference number: 219604
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Pred. No. 16;
2; Mismatches 1; Indels
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   1; Indels
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Pred. No. 15;
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Local Similarity 72.7%;
les 8; Conservative
  Query Match
Best Local Similarity 72.7
Matches 8; Conservative
   119 QLVHSLGGGTG 129
  6 QLMHNLGGGGG 16
   6 QLMHNLGGGGG 16
  Query Match
Best Local S
Matches 8
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Gaps

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A;Cross-references: UNIPROT:049459; UNIPARC:UPI00000A2285; EMBL:AL021749
A;Experimental source: cultivar Columbia; BAC clone F2009
C;Genetics:
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A;Introns: 50/3; 114/1
A;Note: F2009.190
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Matches 7; Conservative
   :| ||||||
241 LHGLGGGGG 249
   8 MHNLGGGGG 16
  Query Match
   ð
  A; Experimental source: strain 99508, UNIPARK::UFIUUUUUCZ6DU; GB:AEU03966; GB:AE003849; NII R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Brinnes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Feranca, A.J.S. submitted to GenBank, June 2000
A; Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigy chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Goliveira, M.C.; de Goliveira, R.C.; Palmieri, D.A; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Sancelli, R.V.; Sawasak, A.J. de M.; de Silva, R.M.; Silva Jr., W.A.; da Silvai, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.; Accenters annotation
  hypothetical protein P2009.190 - Arabidopsis thaliana (Mouse-ear cress)
C;Species: Arabidopsis thaliana (Mouse-ear cress)
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C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
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R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15380
A;Accession: T04621
A;Molecule type: DNA
  Copper homeostasis protein XF1341 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82649
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A83515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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C;Genetics:
A;Genetics:
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   66 VEQSHNRGGGGG 77
   5 IQLMHNLGGGG 15
   ::| | |||||
49 VELCHGLGGGG
  Query Match
Best Local Similarity
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canis famil
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mus musculu
   hypotrichom
hypotrichom
   sus scrofa
homo sapien
brachydanio
brachydanio
  Q91y90 peromyscus
Q91y91 peromyscus
Q80wz2 rattus norv
P04089 rattus norv
Q92016 mus musculu
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equus cabal
   топосетсото
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tetratricho
   trichomitus
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PTHY MACFA
PTHY PIG
Q4VB48 HUMAN
Q5TLZI BRARE
Q6WQ25 BRARE
PTHY BOVIN
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GGWNZ9_9EUKA
GGWPO10_9EUKA
GGWPO12_9EUKA
GGWPO12_9EUKA
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Q9N1V0_HORSE
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Copyright (c) 1993 - 2005
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66.3
66.3
66.3
62.7
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Perfect score:
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  protein
  Sequence:
  Searched:
  Database
  Run on:
  Regult
No.
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oryza sativ fugu rubrip oryza sativ arabidopsis bombyx mori tetraodon n candida alb arabidopsis mus musculu gallus gall mus musculu mus musculu homo sapien homo sapien geobacter s methanobact drosophila drosophila anopheles g anopheles g paxillus in trichonymph xenopus lae gallus gall arabidopsis brachydanio oryza sativ hexamita in oryza sativ rhodopseudo xylella fas valsa cerat brachydanio brachydanio brachydanio Bymbiobacte oryza sativ caenorhabdi tetraodon n anopheles g xenopus lae dicyema sp. suillus bov schizosacch cryptococcu oryza sativ brachydanio oryza sativ trichomonas oryza sativ oryza sativ oreochromia ustilago ma desulfovibr nowakowskie spironucleu morone saxa caenorhabdi trichomonas xenopus tro fugu rubrip trichomonas trichonymph cryptococcu equid herpe 027118 0659m86 0659m86 06533x3 07626x6 084744 086423 0726423 0726423 0726423 0726423 0726423 0726423 0726423 0726423 0726423 0726423 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 0727116 082215 0652K4 0652K4 0660C7 0660C7 0746C5 0746C5 0746C5 0746C5 0746C5 0746C5 0761C6 07 Q25165\_SP1BA Q25165\_SP1BA Q20823\_CAEEL Q76DW0\_9EUKA Q770DW1\_9EUKA Q770Q9\_XENLA TBB6\_CHICK 06W9J4\_FUGRU 09AV00\_ORYSA 09SJA6\_ARATH 0S3N79\_ORYSA 06ND70\_RHOPA CUTC XYLFA 049459 ARATH PIMI BRARE QSC8GI 9PEZI 08CB15\_MOUSE 0SUTU4\_CHICK 0SUTU4\_CHICK 0BUTKB MOUSE 06PCY7\_MOUSE 06PCY7\_MOUSE 06PCY7\_MOUSE 06PCY7\_MOUSE 09H0H0 HUMAN 09H0H0 HUMAN 07493 METTH 0743 METTH 06NS25\_XENLA 050NS25\_XENLA 050N 06K959\_0RYSA 06W024\_BRARE 06Z7117\_TRIVA 02Z7118\_TRIVA 069MSC\_ORYSA 069MSC\_ORYSA 069MSC\_ORYSA 069MSC\_ORYSA 069MSC\_ORYSA 069MSC\_ORYSA 084P3J3\_USTMA 04P3J3\_USTMA 04P3J3\_USTMA 04P3J3\_USTMA 06MNY9\_9EUKA BRARE 227116 TRIVA TBB BOMMO Q4RVA6\_TETNG Q5A586\_CANAL ARATH Q5C8G1 9PEZI Q6DI52\_BRARE 9CAUD Q6BUW8 28JFW9 111099 112090 112090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 1200900 120090 120090 120090 120090 120090 120090 120090 120090 1200900 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090 120090

ALIGNMENTS

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PHTY RAT

PTHY RAT

AC P04089; 063473;

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 04), Last sequence update)

DT 01-NOV-1986 (Rel. 47, Last sequence update)

DT 01-NAY-2005 (Rel. 47, Last sequence update)

DE Parathyroid hormone precursor (Parathyrin) (PTH).

DE Ratus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mamalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.
  Rattus norvegicus (Rat).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Sciurognathi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

NCBI_TaxID=10116;
   Gaps
   Gaps
   TATALNE-SPEAGUENCE.

STRAINE-SPEAGUENCE.

RA MUCLEOTIDE SEQUENCE.

RA MEDLINE-96(79910; PubMed=7588314; DOI=10.1210/en.136.12.5600;

RA MEDLINE-96(79910; PubMed=7588314; DOI=10.1210/en.136.12.5600;

RA SEQUENCE analysis of hypothalamic parathyroid hormone messenger strongering analysis of hypothalamic parathyroid hormone messenger ribonucleic acid ";

Endocrinology 136:5600-5607(1995).

REMBL: 880127; AAP32220.1; -; mRNA.

CO: GO:0005576; C:extracellular region; IEA.

RO: GO:0005576; C:extracellular region; IEA.

InterPro: IPR001415; Phormone activity; IEA.

InterPro: IPR001415; Phormone activity; IEA.

InterPro: IPR001415; Phythorm sub.

PRANTHER; PFRR10541; Phythorm sub.

PRANTHER; PRR50531; PHYTHORM: Sub.

PRANTHER; PRR501932; PHY.

RODOM: PD00081; PRANTHYROID; 1.

RODOM: PROSITE; PS000315; PRANTHYROID; 1.

SNART; SM00087; PHY; 1.

SR PROSITE; PS000315; PRANTHYROID; 1.
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   (1) TOTALDE SEQUENCE.
MUCLEOTIDE SEQUENCE.
MEDLINE=84135846; PubMed=6321505;
Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
   Match 71.1%; Score 59; DB 2; Length 105; Local Similarity 100.0%; Pred. No. 0.2; les 12; Conservative 0; Mismatches 0; Indels
        Query Match 71.1%; Score 59; DB 2; Length 31; Best Local Similarity 100.0%; Pred. No. 0.051; Matches 12; Conservative 0; Mismatches 0; Indels
   01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothalamic parathyroid hormone.
  105 AA
  PRT;
   RESULT 3
980WZZ RAT
1D Q80WZZ;
DT Q80WZZ;
DT 01-UJNN-2003 (TFEMBLrel. 24, DT 01-UJN-2003 (TFEMBLrel. 24, DT 01-UJN-2003 (TFEMBLrel. 24, DT 01-UJN-2003 (TFEMBLrel. 25, DE Hypothalamic parathyroid he wammalia; Butheria; Coc Muridae; Murinae; Rattus. OX NCBI_TAXID=1016; Mr OX NCBI_TAXID=1016;
   1 AVSEIQLMHNLG 12
  22 AVSEIQLMHNLG 33
   1 AVSEIQLMHNLG 12
  13 AVSEIQLMHNLG 24
  Query Match
  д
   ö
   Deromyscus polionotus (Oldfield mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Sigmodontinae; Peromyscus.
NCBI_TaxID=42413;
   Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Sigmodontinae; Peromyscus.
   Gaps
   ö
  Prince KL., December M.J.;
Submittee (KAY-2001) to the EMBL/GenBank/DDBJ databases.
Submittee (KAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF382583, AAK63072.1; -; Genomic_DNA.
HSSP; P01270; 1ZWB.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005576; F:hormone activity; IEA.
InterPro: IPR001415; Parathyrdnm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub.
PROSITE; PS001395; Pthyrhorm_sub; 1.
ProDom; PD010667; Pthyrhorm sub; 1.
ProDom; PD010667; Pthyrhorm sub; 1.
ProDom; PD010667; Pthyrhorm sub; 1.
ProDom; PN01279; Parathyroid; 1.
ProDom; PN01279; A341HYROID; 1.
NOW TER 1 31 31
SEQÜENCE 31 AA; 3461 MW; A208B05772B9B55B CRC64;
   WCLECTIONS SEQUENCE.

WILL AND SEQUENCE.

WILL AND SEQUENCE.

Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.

Brill, APS 193252; AAK63071.1; -; Genomic_DNA.

HSSP; PO1270; LAWB.

GO GO:0005576; C:extracellular region; IEA.

GO; GO:000576; F:hornone activity; IEA.

InterPro; IPR001415; Parathyrd_hrm.

RINERPO; IPR001415; Parathyrd_hrm.

PROMYTER; PTHR10541; Pthyrhorm_sub.

REAM; PP01279; Parathyrdorm_sub; 1.

RODOM; PD010687; Pthyrhorm_sub; 1.

ROSOUTE; PS010687; Pthyrhorm_sub; 1.

ROSOUTE; ROSO135; PARAHYROID; 1.

RONG TER.

1 31

SEQÜENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;
  71.1%; Score 59; DB 2; Length 31; 100.0%; Pred. No. 0.051; tive 0; Mismatches 0; Indels
RESULT 1

Q11Y90_PERMA

TO Q11Y90_PERMA PRELIMINARY; PRT; 31 AA.

AC Q91Y90;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DT 01-UVN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-UVN-2003 (TrEMBLrel. 24, Last annotation update)

DN Name=Pthy.

CN Name=Pthy.

CN Name=Pthy.

CN Muraldae: Sutheria; Buarchontoglires; Glires; Rodentia;

CN Muraldae: Sugmodoutinae; Peromyscus.

CN NCSI TaxID=10042;

RN (11)

RN NUCLEOTIDE SEQUENCE.

RA PILICE (MAY-2001) to the EMBL/GenBank/DDBJ databases

DR HSSP; P01270; 12MB.

DR HSSP; P01270; 12MB.

DR G0; G0:0005576; C:extracellular region; IEA.

DR G0; G0:0005179; Fhormone activity; IEA.

DR InterPro: IPR001415; Parathyrd hrm.

DR InterPro: IPR001415; Parathyrd hrm.

DR PRODINGS PRIMINOSA1; Phythorm sub; 1.

PRODINGS PRODINGS PERMINOSD1: 1.

FT NON TER 1 1 1

FT NON TER 3 31

SQUENCE 31 AA; 3461 MW; A208BBS5B CRC64;
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31 AA; 3461 MW; A208B0E772B9B55B CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone (Fragment).
  31 AA.
  PRT;
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O11791 PERPL

ID G51791 PERPL PRELIMINARY;

AC 091791;

DT 01-DEC-2001 (TrEMBLrel. 19,

DE PARATHYCOIG HORMONE (Fragment of the percent of
  Local Similarity 100. es 12; Conservative
   1 AVSEIQLMHNLG 12
   13 AVSEIQLMHNLG 24
   Query Match
   Matches
  qq
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RESULT O
  SOLITION SOL
  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
  TISSUE=Parathyroid;
Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
  Endocrinology 136:5600-5607 (1995).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
"Gene encoding parathyroid hormone. Nucleotide sequence of the rat gene and deduced amino acid sequence of rat preproparathyroid hormone.";
  NUCLEOTIDE SEQUENCE OF 32-115.
STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
NULLEY M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger
  -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
  71.1%; Score 59; DB 1; Length 115;
  Schmelzer H.-J., Gross G., Widera G., Mayer H.; "Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
  7B434CFCA528B230 CRC64;
  C -> Y (in Ref. 3).
A -> T (in Ref. 3).
V -> I (in Ref. 3).
V -> G (in Ref. 3).
   Parathyroid hormone.
  HSSP, P01270; 1ZWB.
Ensembl; ENSRNOG0000014318; Rattus norvegicus.
RGD; 3440; Pth.
  Pred. No. 0.22;
  100.0%; Pred. ...
   EMBL; KO1268; AAA41979.1; -; Genomic_DNA.
EMBL; XO5721; CAA29192.1; -; mRNA.
EMBL; M54875; AAA57156.1; -; mRNA.
EMBL; SO127; -; NOT_ANNOTATED_CDS; mRNA.
PIR; AO5091; AO5091.
  InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR003626; PTH related.
InterPro; IPR003625; PTH related.
InterPro; IPR003625; PTH related.
PANTHER; PTHR10541; Pthyrhorm_sub; IPRSP01279; Parathyroid; I.PIRSF; PIRSF001832; PTH; 1.ProDom; PD013225; PTH related; I.ProDom; PD01687; Pthyrhorm_sub; I.SMART; SM00087; PTH; 1.PR031TE; PS00335; PARATHYROID; I.
   Adv. Gene Technol. 21:228-229(1984).
  Biol. Chem. 259:3320-3329(1984)
  MEDLINE=87316938; PubMed=3628009;
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62
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  ribonucleic acid.";
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  SEQUENCE
  removed.
  CONFLICT
  CONFLICT
  PROPEP
  SIGNAL
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Gaps

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0; Indels

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MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

M. Klausber R. D., Feingold E. A., Grouse L. H., Derge J. G.,

M. Klausher R. D., Collins F. S., Wagner L. Schemmen C. M., Schuler G. D.,

Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,

M. Diatchenko L., Marusina K., Parmer A. A., Rubin G. M., Hong L.,

Brownstein M. J., Usdin T. B., Toshhyuki S., Carninci P., Prange C.,

Raha S. B., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,

Rosak S. A., McEwan P. J., McKerran K. J., Malek J. A., Gunaratne P. H.,

M. Richards S., Worley K. C., Hale S., Garcia A. M., Gubbs R. A.,

M. Halton B., Retteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,

Mhiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,

Makealey R. W., Touchman J. W., Gremutz J., Myers R. M.,

Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M.,

Schnerch A. Schein J. E., Jones S., M., Marra M. A., Schnerth human
  Generation and initial analysis of more than 15,000 full-length human
   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Mus.
  Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M., "Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
  Submitted (JUL_2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AF066075; AAC99656.1; -; Genomic_DNA.
EMBL; BC099456; AAH99456.1; -; mRNA.
  Potential.
parathyroid hormone.
; DA43FABBCB4E2FD9 CRC64;
   01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
  Ensembl: ENSWUSGO0000059077; Mus musculus.
MGI; MGI:97799; Pth.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005179; F:hormone activity; IDA.
GO; GO:0006874; P:calcium ion homeostasis; TAS.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003625; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
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12825 MW;
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Q9Z0L6_MOUSE PRELIMINARY;
Q9Z0L6;
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  32 1
115 AA;
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  NUCLEOTIDE SEQUENCE.
  NUCLEOTIDE SEQUENCE.
   HSSP; P01270; 1ZWB.
  NCBI_TaxID=10090;
  TISSUE=Thyroid;
NIH MGC Project;
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   STRAIN=129/Sv;
  SEQUENCE
  Name=Pth;
   Signal.
SIGNAL
   SMART;
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   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
  Gaps
  Gaps
   Shiue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F., Murray J.D., Bouling A.T.;
Submitted (MAR-1919) to the EMBL/GenBank/DDBJ databases.
EMBL, AF134233, AAF62347.1; -; Genomic_DNA.
EMBL, AF13423, AAF62347.1; -; Genomic_DNA.
EMBL, AF13423; AAF62347.1; -; Genomic_DNA.
GO; GO:0005170; EMI.
GO; GO:0005179; F:hormone activity; IEA.
InterPro; IPR001415; Parathyrd,hrm.
InterPro; IPR00145; Parathyrd,hrm.
InterPro; IPR003625; Phythorm sub.
   Equus caballus (Horse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia, Buteria, Laurasiatheria, Perissodactyla, Equidae, Equus.
  [1] WUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

MEDILINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;

Cactano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,

Bowling A.T., Murray J.D.; the horse (Equus caballus).";

A comparative gene map of the horse (Equus caballus).";

[2] NUCLECTIDE SEQUENCE.
   21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
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  ö
Score 59; DB 2; Length 115; Pred. No. 0.22; 0; Mismatches 0; Indels
  Score 56; DB 2; Length 86;
Pred. No. 0.48;
1; Mismatches 0; Indels
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   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone (Fragment).
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   115 AA
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   PRT;
  PROSITE; PS00335; PARATHYROID; 1.
  Query Match
PBest Local Similarity 100.0%;
Matches 12; Conservative 0
   67.5%;
Local Similarity 91.7%;
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Q9N1V0;
   1 AVSEIQLMHNLG 12
   STANDARD;
  1 AVSEIQLMHNLG 12
   AVSEIQLMHNLG 43
   SVSEIQLMHNLG 14
   Homo sapiens (Human)
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   NCBI_TaxID=9606;
   SM00087
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SEQUENCE
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PTHY_HUMAN
ID PTHY HUMAN
ID PTHY HUMAN
ID 13-AUG
DT 13-AUG
DT 13-AUG
DN Name=P
OC BUKATY
OC Mammall
OC Mammall
OC NON NBM
  Best Loc
Matches
   RESULT 6

OGNIVO HOO

10 OGNIVO HOO

OGNIVO HOO

OGNIVO HOO

OGNIVO HOO

OGNIVO HOO

OGNIVO HOO

OGNIVO HOO

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   hypoparathyroidism.";
J. Clin. Endocrinol. Metab. 84:3792-3796 (1999).
J. Clin. Endocrinol. Metab. 84:3792-3796 (1999).
J. FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
J. SUBCELLULAR LOCATION: Secreted.
J. DISEASE: Defects in PTH are a cause of familial isolated hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal dominant and recessive forms of hypoparathyroidism.
J. SIMILARITY: Belongs to the parathyroid hormone family.
Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.; "Investigation of the solution structure of the human parathyroid hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and molecular dynamics calculations.";
   STRUCTURE BY NMR OF 32-70.
MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
"Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
Biochem. Biophys. Res. Commun. 267:213-220(2000).
  Sunthornthepvarakul T., Churesigaew S., Ngowngarmratana S., "A novel mutation of the signal peptide of the preproparathyroid hormone gene associated with autosomal recessive familial isolated
   STRÜCTURE BY NWR OF 32-68.
MEDLINES-953180684; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
MATX U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.
   MEDLINE-93345518; PubMed-8344299;
Barden J.A., Cuthbertson R.M.;
"Stabilized NMR structure of human parathyroid hormone(1-34).";
   "Structure of human parathyroid hormone 1-37 in solution."; J. Biol. Chem. 270:15194-15202(1995).
  MEDLINE=91009811; PubMed=2212001;
Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.
Kronenberg H.M.;
   "Mutation of the signal peptide-encoding region of the preproparathyroid hormone gene in familial isolated
   Unassigned DNA
   EMBL; J00301; AAA60215.1; -; Genomic_DNA.
EMBL; V00597; CAA23843.1; -; mRNA.
   nypoparathyroidism.";
J. Clin. Invest. 86:1084-1087(1990)
   Eur. J. Biochem. 215:315-321(1993)
   Biochemistry 30:6936-6942(1991)
   CAA01956.1; -;
   X-ray; A/B=32-65.
Model; A=32-65.
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NWR; G=32-65.

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NWR; G=32-65.

NWR; G=33-65.
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   PubMed=10523031;
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   GO: GO: 0005576; C:extracellular region; NAS.
GO: GO: 0005179; P: hormone activity; TAS.
GO: GO: 0005179; P: hormone activity; TAS.
GO: GO: 0006874; P: calcium ion homeostasis; NAS.
GO: GO: 0006874; P: callcium ion homeostasis; NAS.
GO: GO: 0007267; P: callcium ion homeostasis; NAS.
GO: GO: 0007267; P: callcium ion properties; TAS.
GO: GO: 0007186; P: prediction of apoptosis by hormones; TAS.
GO: GO: 0001501; P: skeletal development; TAS.
InterPro: IPR001415; Parathyrd hrm.
InterPro: IPR00341; Pthyrhorm_sub.
PANTHER: PFTRR10541; Pthyrhorm_sub.
PANTHER: PFTRR10541; Pthyrhorm_sub; 1.
   Parathyroid hormone.

C -> R (in FIH; dominant; leads to inefficient processing of the precursor).

Frid=VAR_006047.
   S -> P (in FIH) recessive, might lead to inefficient processing of the precursor)/FIId=VAR_018464.
   Gaps
   NUCLEOTIDE SEQUENCE.
Malaivijtnond S., Takenaka O.;
"Nucleotide sequences of parathyroid gene in five species of macaque of Thailand.";
  salts in
  3D-structure; Direct protein sequencing; Disease mutation; Hormone;
  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
   ;
   J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
-!- FUNCTION: PTH elevates calcium level by dissolving the bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
   67.5%; Score 56; DB 1; Length 115; ilarity 91.7%; Pred. No. 0.67; Conservative 1; Mismatches 0; Indels
  64
12861 MW; 849015736A6E5597 CRC64;
  Q9XT35;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
  N -> D (in Ref. 6)
   115 AA
   Cercopithecidae; Cercopithecinae; Macaca.
              Ensembl; ENSG0000152266; Homo sapiens.
HGNC; HGNC:9606; PTH.
  Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
Probon; PD010687; Pthyrhorm_sub; 1.
SWART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
   1 AVSEIQLMHNLG 12
  32 SVSEIQLMHNLG 43
   STANDARD;
   25
31
115
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   23
   107
  34
115 AA;
   Local Similarity
les 11; Conser
  NCBI_TaxID=9541;
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32
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  107
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  CONFLICT
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  Query Match
   CHAIN
VARIANT
  VARIANT
   Signal.
   SIGNAL
  PTHY_MACFA
  Best Loc
Matches
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Direct protein sequencing; Hormone; Signal. SIGNAL
  HSSP; P01270; IBWX.
HSSP; P01270; IBWX.
INTERPLO: IRROD1415; PRINThorm_sub.
INTERPLO: PR0013625; Pthyrhorm_sub.
PANTHER; PTHA10541; Pthyrhorm_sub; 1.
PIRSP; PR01279; PRINTHOIG, 1.
PIRSP; PIRSP(001832; PTH; 1.
SWART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
  EMBL; X05722; CAA29193.1; -; mRNA.
PIR; B26806; PTPG.
   CHAIN 32 115 P
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TISSUE=PCR rescued clones;
   1 AVSEIQLMHNLG 12
  32 SVSEIQLMHNLG 43
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  Query Match
   HUMAN
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the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is removed.
   Gaps
  PROTEIN SEQUENCE OF 32-115.

MEDLINE=74253317; PubMed=4840833;

Sader R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,

Potts J.T. Jr.,

"The amino acid sequence of porcine parathyroid hormone.";

"The amino acid sequence of porcine parathyroid hormone.";

Bocheniarry 13:1994-1999(1974).

-I- FUNCTION: PIH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

-I- SUBCELLUIAR LOCATION: Secreted.

-I- SIMILARITY: Belongs to the parathyroid hormone family.
   Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
   PROTEIN SEQUENCE OF 26-115.

MEDLINE=76018954; PubMed=1164500;

Chu L.L.H., Huang W.-Y., Littledike B.T., Hamilton J.W., Cohn D.V.;

Chu protaine proparathyroid hormone. Identification, blosynthesis, and partial amino acid sequence..;

Biochemistry 14:3631-3635(1975).
   ;
0
   Score 56; DB 1; Length 115;
Pred. No. 0.67;
1; Mismatches 0; Indels
   (1)

NUCLECTIDE SEQUENCE.

MEDLINE=87316938; PubMed=3628009;
Schmelzer H.-J., Gross G., Widera G., Mayer H.;
Schmelzer esquence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
  By similarity.
By similarity.
By stanthyroid hormone.
RC2500EP24BE5597 CRC64;
  21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
   EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
HSSP; P01270; 1ET.
ILLGEPPC; IRP001415; Parathyrd_hrm.
ILLGEPPC; IRP001415; Parathyrd_hrm.
ILLGEPPC; IRP001415; Parathyrd_maub.
PAWHER; PIRHAI0541; Pethyrhorm_sub; 1.
PERSF; PIRSF001832; PTH; 1.
PROSITE; PS001835; PTH; 1.
PROSITE; PS00335; PTH; 1.
PROSITE; PS00335; PRATHYROID; 1.
PROSITE; PS00335; PARATHYROID; 1.
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Local Similarity 91.7%;
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   Query Match
  Matches
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NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

MEDILINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang L.,

And Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A posters M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Pothiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wickernan W.J., Mallek J.A., Gunsardne P.H.,

Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hullyk S.W.,

A Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hullyk S.W.,

A Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hullyk S.W.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
   ö
   Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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NIH MGC Project;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases:
EMBL; BC096143; AAH96143.1; -; mRNA.
EMBL; BC096144; AAH96141; -; mRNA.
Parathyroid hormone.
9FE8BCDE614BAC16 CRC64;
  OGVB46 HUMAN PRELIMINARY; PRT; 115 AA.
14.784B .
13.5EP-2005 (TrEMBLrel. 31, Created)
13.5EP-2005 (TrEMBLrel. 31, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyroid hormone, preproprot
   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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parathyroid hormone."
Gene 28:319-329(1984)
  NCBI_TaxID=7955;
   PTHY BOVIN
  SEQUENCE
   PTHY_BOVIN
   RESULT 13
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  Gaps
   Name=pth);
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Caniata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafata; Craniata; Vertebrata; Euteleostomi;
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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  A NORDOM, GENDAMAL,

OKADE M., GENDAMAL,

I'The origin of the parathyroid gland.";

Proc. Nail. Acad. Sci. US.A. 101:17716-17719(2004).

ENBL; AB175679; BAD72832.1; -; mRNA.

ZFIN; ZDB-GENE-040623-1; pthl.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0005179; F:hormone activity; IEA.

InterPro; IPR001415; Parathyrd.hrm.

InterPro; IPR001415; Parathyrd.hrm.

PANTHER; PTHR.0541; Pthyrhorm_sub;

RAMRT; SM00087; PTH; 1.
EMBL; BC096145; AAH96145.1; -; mRNA.
EMBL; BC096142; AAH96142.1; -; mRNA.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001625; Pthyrhorm_sub.
Pfam; PF01279; Parathyrorid; 1.
ProDom; PF01279; Parathyrorid; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
PROSITE; S000087; PTH; 1.
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  01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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  1; Mismatches
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05-JUL-2004 (TrEMBLrel. 27, Last an
Parathyroid hormone ligand type-1.
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QSTLZ1;
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Best Local Similarity 83.3'
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Q6WQ25;
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AC QGWQ2
DT 05-JU
DT 05-JU
DT 05-JU
DE Parat
GN Brach
OC Bukar
OC Sukar
  Matches
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A Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
A Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
A Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
A lastepe M., Rubin D.A., Juppner H.;
Indentification and characterization of two parathyroid hormone-like
T molecules in zebrafish.";
I Endocrinology 145:1634-1639(2004).
R EMBL, AZ725669; AA016566.1; -; mRNA.
R ZFIN; ZBB-GENE-040623-1; ptl. -; mRNA.
R ZFIN; ZBB-GENE-040623-1; ptl. -; mRNA.
GO; GO:0005179; F:hormone activity; IEA.
R InterPro; IPR001415; Parathyrof hrm.
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R Probom; PP01279; Parathyroid; 1.
R Probom; PP01279; PTH; 1.
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MEDLINE=80056617; PubMed=388425;
Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
Frontenberg J.T. Jr., Rich A.,
"Cloning and nucleotide sequence of DNA coding for bovine
   NUCLEOTIDE SEQUENCE.
MEDLINE-82037785; PubMed-6170060;
Weaver C.A., Gordon D.F., Kemper B.;
"Introduction by molecular cloning of artifactual inverted sequences at the S' terminus of the sense strand of bovine parathyroid hormone
   Gaps
  MEDLINE-83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8; Weaver C.A., Gordon D.F., Kemper B.; "Nucleotide sequence of bovine parathyroid hormone messenger RNA."; Mol. Cell. Endocrinol. 28:411-424(1982).
   NUCLEOTIDE SEQUENCE.
MEDINES=84264481, Pubmed=6086460, DOI=10.1016/0378-1119(84)90149-5;
WREDINES=8426481, Pubmed=6086460, DOI=10.1016/0378-1119(84)90149-5;
WREDINES=84266481, Pubmed=6086460, DOI=10.1016/0378-1119(84)90149-5;
WREDINES-84266481, Pubmed=6086460, DOI=10.1016/0388-1196(84)90149-5;
WREDINES-84266481, Pubmed=60866681, Pubmed=6086688-1196(84)90149-5;
WREDINES-8426667, Pubmed=608667, Pubmed=60867, Pubme
   Bos taurus (Bovine).
Bukaryota; Metazota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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  11690 MW; SAA7A84FF4110764 CRC64;
  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MRY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
  preproparathyroid hormone.";
Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979)
   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981)
   115 AA
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   1 AVSEIQLMHNLG 12
   36 AVNEVOLMHNLG 47
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FSJ PROTEIN SEQUENCE OF 26-115.
PROTEIN SEQUENCE OF 26-115.
MEDLINE-74142666; PubMed44522780;
Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
Hamilton J.W., Niall H.D., Jacobs G.W., Keutmann H.T., Potts J.T. Jr.,
"The N-terminal amino-acid sequence of bovine proparathyroid
hormone.",
hormone.",
Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
   PERUCTURE BY NMR OF 32-68.

MEDIATE-20090619; PubMed-10623601; DOI=10.1006/bbrc.1999.1958;

MEDIATE-20090619; PubMed-30623601; DOI=10.1006/bbrc.1999.1958;

MEX U.C., Adermann K., Bayer P., Foresmann W.-G., Rosch P.;

"Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";

Blochem. Biophys. Res. Commun. 267:213-220(2000).

-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
  SYNTHESIS OF 32-65.

BEDLINE-11091588; PubMed=4322265;
POELE J. T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
"Synthesis of a biologically active N-terminal tetratriacontapeptide
of parachyroid hormone."
Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
  PROTEIN SEQUENCE OF 32-115.

MEDLINE-71056162; PubMed=5531031;

Niall H.D., Keutemann H.T., Sauer R., Hogan M.L., Dawson B.F.,

Aurbach G.D., Potts J.T. Jr.;

The amino acid sequence of bovine parathyroid hormone I.";

Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
  InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Pfam; PF01279; Parathyroid; 1.
ProDom; PF010687; PTH; 1.
PROSITE; PS000315; PTH; 1.
PROSITE; PS000315; PARATHYROID; 1.
PROSITE; PS000315; PARATHYROID; 1.
PROSITE; PS000315; PARATHYROID; 1.
PROPEP 25
  63
12980 MW; 2ED246B348880710 CRC64;
  PROTEIN SEQUENCE OF 32-115.
MEDLINE-71063634; PubMed=5275384;
Brewer H.B. Jr., Ronan R.,
"Bovine parathyroid hormone: amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
   Parathyroid hormone. V -> G (in Ref. 4).
  EMBL; V00106; CAA23439.1; -; mRNA.
EMBL; J000024; AAA30747.1; -; mRNA.
EMBL; K01938; AAA30749.1; -; Genomic_DNA.
EMBL; M25082; AAA30749.1; -; mRNA.
PIR, A24949; PTBO.
   31
115
106
40
  61
115 AA;
  CHAIN
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  TURN
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SEQUENCE
  removed
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   NUCLEOTIDE SEQUENCE.
MEDLINE-89219100; PubMed=2710135;
Russell J., Sherwood L.M.;
"Nucleotide sequence of the DNA complementary to avian (chicken)
preproparathyroid hormone mRNA and the deduced sequence of the hormone
  01-ARR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (PTH).
Name=PTH;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
   Gaps
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0
  Score 53; DB 1; Length 119;
Pred. No. 2.1;
Score 55; DB 1; Length 115;
Pred. No. 0.96;
0; Mismatches 1; Indels
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B309D8E772997F6E CRC64;
   EMBL, M16604; AAA49093.1; -; mRNA.
EMBL, M34937; A34937.
PIR, A34937; A34937.
Ensembl; ENSCALGO000005358; Gallus gallus.
Interpro; IPR001415; Parathyrd hrm.
Interpro; IPR00366; PTH related.
Interpro; IPR003625; Pthyrhorm sub.
PANTHER, PTHR10541; Pthyrhorm sub.
PERNY, PIRSF001932; PTH; 1.
  119 AA.
   ProDom; PD033225; PTH_related; 1. ProDom; PD013225; PTH_related; 1. SMART; SM00087; PTH; 1. PROSITE; PS00335; PARATHYROID; 1. Hormone; Signal. 25
   PRT;
  precursor.";
Mol. Endocrinol. 3:325-331(1989).
   119 Pa
   63.9%;
        Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
   1 AVSEIOLMHNLG 12
   32 AVSEIQFMHNLG 43
   STANDARD;
   32
119 AA;
  Query Match
Best Local Similarity
  Gallus.
NCBI_TaxID=9031;
   CHICK
   SEQUENCE
  removed.
   PTHY C
   PTHY_CHICK
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
  Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
   STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.012671499;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of Myperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
  Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
  DB 1; Length 115;
  1; Indels
   By similarity.
By similarity.
Parathyroid hormone.
, 80CD557CC6AlA47E CRC64;
   Last sequence update)
Last annotation update)
05-JUL-2004 (Rel. 44, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
  394 AA
  62.7%; Score 52; DB : 83.3%; Pred. No. 2.8;
  1; Mismatches
  InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Pthyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub; 1.
Ptam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; PD010687; Pthyrhorm sub; 1.
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
Acetyl-CoA acetyltransferase.
  EMBL; AF309967; AAG30545.1; -; mRNA.
   25 By
31 By
115 Pa
12921 MW;
  QBTULL METKA PRELIMINARY;
  OrderedLocusNames=MK1378;
  Query Match
Best Local Similarity 83.3
Matches 10; Conservative
   1 AVSEIQLMHNLG 12
  SVSEIOFMHNLG 43
   Methanopyrus kandleri
   NUCLEOTIDE SEQUENCE.
  115 AA;
   HSSP; P01268; 1ZWC
  NCBI_TaxID=2320;
  Felinae; Felis.
NCBI_TaxID=9685;
   Methanopyrus
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  removed.
   Q8TVL1_METKA
   OSTVL1;
  PROPEP
   SIGNAL
  RESULT 17
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  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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       Gaps
   MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C; Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W., Capen C.C.;
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
  "Sequences of the cDNAs encoding canine parathyroid hormone-related
  Gene 160:241-243(1995).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in
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  bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
   62.7%; Score 52; DB 1; Length 115; 83.3%; Pred. No. 2.8;
       Indels
   Indels
  By similarity.
By similarity.
Parathyroid hormone.
FC38F77F1C8CFE56 CRC64;
   ;;
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  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10.MAY-2005 (Rel. 47) Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH)
   HSSP; P01268; 1ZWC.
Ensembl; ENSCAFG00000008177; Canis familiaris.
  115 AA
  115 AA.
  Pred. No. 2.8;
1; Mismatches
       2; Mismatches
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InterPro; IPR003625; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub, 1.
Pfan, PF01279; Parathyroid; 1.
PRSF, PRRSF001832; PTH, 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
  PRT;
  PRT;
   profein and parathyroid hormone.";
   EMBL; U15662; AAA82584.1; -; mRNA.
  PROSITE; PS00335; PARATHYROID; 1.
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AC Q92L67;
DT 05-JUL-2004 (Rel. 44, Created)
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   1 AVSEIQLMHNLG 12
   SVSEIQFMHNLG 43
  SVSEMQLMHNLG 43
       10; Conservative
                                       1 AVSEIQLMHNLG 12
  STANDARD;
  25
31
  115
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  PIR; JC4202; JC4202.
   SMART; SM00087; PTH;
   NUCLEOTIDE SEQUENCE.
  IISSUE=Parathyroid;
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   NCBI_TaxID=9615;
   Hormone; Signal
  PTHY CANFA P52212;
   SEQUENCE
   Query Match
  Name=PTH
   removed.
   PROPEP
  SIGNAL
  Canis
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01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Novel protein (Fragment)
Name-CTYMNSP00000001188; ORFNames=RP23-5084.2-005;
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalla; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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NCBI_TAXID=10090;
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  WICLEOTIDE SEQUENCE.
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Phillimore B.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL592065; CAIZ5664.1; -; Genomic_DNA.
NON TER 140
A3, 15587 MW, F5108D76C2FFD8EE CRC64;
  1 AVSEIQLMHNLGGGGG 16
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  MOUSE
   RESULT 20
OSSXZS MOU
DO SSXZS
MOU
DO SSXZ
DT 01-FE
DT 01-FE
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   No. CENTRAINEAXA;

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In Song D., Gloeckner G., Rajandream M.-A.,

Sucgang R., Berriman M., Song J., Olsen R., Saafranski K., Xu Q.,

Sucgang R., Berriman M., Song J., Olsen R., Saafranski K., Xu Q.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

A Bankier A.T., Lehmann R., Hamlin N., Davise R., Gaudet P., Fey P.,

Pailcher K., Chen G., Saunders D., Sodergren E., Davis P.,

Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

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Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Rerhornou A., Nie X., Wall R., Morio T., Rost R., Churcher C.,

Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

Nauzny D., Moutier T., Pann A., Lu M., Hangavelu M., Johnson D., Lindsay R.,

Loulseged H., Mungall R., Oliver K., Price C., Quail M.A.,

Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,

Na J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,

Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,

Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,

A Milliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;

"The genome of the social amoeba Dictyostelium discoideum.";

"The genome of the social amoeba Dictyostelium discoideum.";

"The GAUTION: The sequence shown here is derived from an EMBLY Cox B.C.,

BABL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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  / Match 60.2%; Score 50; DB 2; Length 394; Local Similarity 64.3%; Pred. No. 23; and see 9; Conservative 2; Mismatches 3; Indels
  Match 59.0%; Score 49; DB 2; Length 885; Local Similarity 55.0%; Pred. No. 84; tes 11; Conservative 2; Mismatches 1; Indels
                   Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
BMBL, AE010431; AAM025591.1; -; Genomic DNA.
GO; GO:0016740; F:transferse activity; IBA.
InterPro; IPR002155; Thiolase.
Pfam; PF02803; Thiolase C; 1.
Pfam; PF0108; Thiolase C; 1.
Complete proteome; Transferse.
SEQUENCE 394 AA; 42063 MW; A816CFFFPDE634E4 CRC64;
  EMBL, AARIO1000009; EAL/3219.1; -; Genomic_DNA.
Hypochetical protein.
SEQUENCE 885 AA; 97636 MW; 7F56B9DFBC85BEBA CRC64;
  Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
  preliminary data.
   885 AA.
  PRT;
   3 SEIOLMH-----NLGGGGG 16
   370 AEIGLTHNVGGSGG 383
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  DICDI PRELIMINARY;
  Hypothetical protein.
ORFNames=DDB0189350;
   NUCLEOTIDE SEQUENCE.
   Query Match
  Query Match
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  RESULT 18
OS 508 9 DIC
10 508 508 9 DIC
05 508 9 DIC
05 508 9 DIC
07 508 9 DIC
08 13 - SE
08 18 18 - SE
08 18 
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PRT;

RESULT 19 Q5SXZ6 MOUSE ID Q5SXZ6 MOUSE PRELIMINARY; AC Q5SXZ6;

SPIQLIHPNLDSPNVGGGGG 176

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  Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Bumanyota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,

Muridae, Murinee, Mus.
  Gaps
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   57.8%; Score 48; DB 2; Length 190;
62.5%; Pred. No. 21;
iive 0; Mismatches 6; Indels
  Phillimore B.; Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases. EMBL, AL592065; CAI25865.1; -; Genomic_DNA. NON TER 190 As; 20892 MW; FODC4841A26B53C5 CRC64;
  O1-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Novel protein (Fragment)
Name=OTIMUSPO0000001189; ORFNames=RF23-50E4.2-007;
  Search completed: November 21, 2005, 16:42:55 Job time : 238 secs
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  92 ASKEQQLRHKLGGGSG 107
   1 AVSEIQLMHNLGGGGG 16
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QSSXZS;
   Query Match
Best Local Similarity 62.59
watches 10; Conservative
  NUCLEOTIDE SEQUENCE.
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                      November 21, 2005, 16:38:20; Search time 46 Seconds (without alignments) 28.757 Million cell updates/sec
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Sequence 8, A
Sequence 48,
   Sequence 5, 1
Sequence 5, 1
Sequence 11,
  Sequence 31
Sequence 6,
Sequence 9,
Sequence 15
Sequence 5,
Sequence 22
Sequence 23
Sequence 23
Sequence 23
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Sequence 4
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Copyright (c) 1993 - 2005 Compugen Ltd.
  US-09-730-174A-5

US-09-471-379-5

US-09-448-867-5

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US-09-448-867-9

US-09-448-867-9

US-10-157-076-5

US-10-157-076-9

US-09-448-867-4

US-09-448-867-4

US-09-448-867-8

US-09-448-867-8

US-09-448-867-8

US-09-448-867-8

US-09-448-867-8

US-09-448-80-9

US-09-448-105-9

US-09-448-105-9

US-09-448-105-9

US-09-447-800-5

US-09-843-221A-25

US-09-843-221A-11

US-09-843-221A-11
  -09-843-221A-25
   Total number of hits satisfying chosen parameters:
   572060 segs, 82675679 residues
   SUMMARIES
  Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                             using sw model
  BLOSUM62
Gapop 10.0 , Gapext 0.5
   1 avseiglmhnlggggg 16
   DB seq length: 0
DB seq length: 200000000
  DB
  Length
                             protein search,
  Issued
  SEQ-NEW
  Query
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   Post-processing:
   Title:
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S-08-691-647C-2 S-08-691-647C-3 S-08-691-647C-4 S-08-691-647C-6 S-08-991-647C-6 S-08-904-760B-1 S-08-904-760B-2

US-08-691-647C-1 US-08-691-647C-2 US-08-691-647C-3

Sequence

US-09-843-221A-125 US-09-843-221A-126 US-09-843-221A-126 US-09-843-221A-166 US-08-262-495C-4

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S-00-904-760B-3 S-08-904-760B-4 S-08-904-760B-5 S-08-904-760B-8 S-08-904-760B-1 
Sequence Sequence Sequence

US-09-536-785A-4 US-09-536-785A-5

Sequence Sequence

-08-904-760B-21 -08-904-760B-32

Gaps

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Sequence 11, Application US/09730174A

Batent No. 6838264

GERREAL INFORMATION:
GERREAL INFORMATION:
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hox FILE REPERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 11
LENGTH: 15
   ; FEATURE; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-1148-11
   Query Match 71.1%; Score 59; DB 2; Length 15; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 12; Conservative 0; Mismatches 0; Indels
  TYPE: PRT
ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity 100.
Best Local 2; Conservative
   1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
  1 AVSEIOLMHNLG 12
   1 AVSEIQLMHNLG 12
  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-867-5
  Dp
   g
  Sequence 5. Application US/09730174A

Batent No. 6838264

GENERAL INFORMATION:

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HC FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT PILING DATE: 2000-12-05

SEQ ID NOS: 12

LENGTH: 12
   ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-5
   ö
   .;
0
  RESULT 2
US-09-421-379-5
is Sequence 5, Application US/09421379
j Patent No. 649562
is GREEAL INFORMATION:
j APPLICANT: Gardella, Thomas J.
j APPLICANT: Gardella, Thomas J.
j APPLICANT: Gardella, Thomas J.
j APPLICANT: Brotts, John T.
j APPLICANT: Unuppner, Harral
j TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Bioactive Peptide (PTH) and Parathyroid
j TITLE OF INVENTION: Bioactive Peptide (PTH) and Parathyroid
j TITLE OF INVENTION: Hormone.Related Peptide (PTHrP)
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
j EARLIER RILING DATE: 1999-10-20
j SARLIER FILING DATE: 1998-10-22
j NUMBER OF SEQ ID NOS: 13
j SOFTWARE: PatentIn Ver. 2.0
j SEQ ID NO 5
j LENGTH: I.
   Gaps
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   ; FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-421-379-5
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   Query Match 71.1%; Score 59; DB 2; Length 14; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 12; Conservative 0; Mismatches 0; Indels
  Query Match 71.1%; Score 59; DB 2; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0088; Matches 12; Conservative 0; Mismatches 0; Indels
   ALIGNMENTS
   TYPE: PRT
ORGANISM: Artificial Sequence
  TYPE: PRT ORGANISM: Artificial Sequence
   1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
  RESULT 3
, US-09-730-174A-11
  RESULT 1
US-09-730-174A-5
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WESOLI A PAPICATION US/09448867

Sequence 5, Application US/09448867

Sequence 5, Application US/09448867

PAPELICANT BRINGHURST, F. RICHARD

APPLICANT: PARASU, HISASHI

APPLICANT: TARASU, HISASHI

APPLICANT: POTTS JR., JOHN T.

TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

TITLE OF INVENTION: AND USE

TITLE OF INVENTION: WIMBER: US/09/448,867

CURRENT APPLICATION NUMBER: US/09/448,867

CURRENT APPLICATION NUMBER: 06/109,938

EARLIER FILING DATE: 1999-11-24

SEALIER PELLOR DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

SSOTUD NOS: 13

LENGTH: 27
  ö
  RESULT 5

US-09-448-867-9

Sequence 9, Application US/09448867

Patent No. 641733

GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
APPLICANT: POTTS JR., JOHN T.
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
TITLE REFERENCE: 0609-4640001
CURRENT APPLICATION NUMBER: US/09/448,867
  ö
   71.1%; Score 59; DB 2; Length 27; 100.0%; Pred. No. 0.02; 1ive 0; Mismatches 0; Indels
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Gaps

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Sequence 9, Application US/10157076
; Sequence 9, Application US/10157076
; Patent No. 68030131
; GENERAL INFORMATION:
; APPLICANT: Bringhurst, F. Richard
; APPLICANT: Takasu, Hisabhi
; APPLICANT: Takasu, Hisabhi
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
; PILE REFERENCE: 0609,4440002
; CURRENT FILING DATE: 1099-1125
; CURRENT FILING DATE: 1099-1125
; PRIOR FILING DATE: 1999-11-25
; NUMBER: OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENTH: 27
  Sequence 4, Application US/09448867

Sequence 4, Application US/09448867

Patent No. 641733

GENERAL INFORMATION:

APPLICANT: BRIGHURGY, F. RICHARD

APPLICANT: TAKASU, HISASHI

APPLICANT: TAKASU, HISASHI

APPLICANT: GARDELLA, THOWAS J

TITLE OF INVENTION: HUWAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

TITLE OF INVENTION: AND USE

FILE REFERENCE: 0609.4640001

CURRENT APPLICATION NUMBER: US/09/448,867

CURRENT FILING DATE: 1999-11-24

EARLIER PFLING DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN VEY: 2.1

SEQ ID NO 4

LENGTH: 28

TENDER PATENTION NUMBER: 60/109,938
   Query Match

71.1%; Score 59; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 12; Conservative 0; Mismatches 0; Indels
  Length 27;
   0; Indels
  Score 59; DB 2;
Pred. No. 0.02;
   71.1%; 500.100.0%; Pred. No. 0. 0. Mismatches
NUMBER OF SEQ ID NOS: 13
SOFWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 27
  1 AVSEIQLMHNLG 12
   Best Local Similarity 100.
Matches 12; Conservative
  1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
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  TYPE: PRT
ORGANISM: Homo sapiens
   ORGANISM: Homo sapiens
   TYPE: PRT;
CORGANISM: Homo sapiens
US-10-157-076-5
  RESULT 8
US-10-157-076-9
   Query Match
   ઠે
  셤
   ઠ
  APPLICANT: Bringhurst, F. Richard
APPLICANT: Takaeu, Hissehi
APPLICANT: Takaeu, Hissehi
APPLICANT: Takaeu, Hissehi
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Optis, John T. Jr.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
FILE REPERENCE: 0609.4640002
CURRENT PAPLICATION NUMBER: US 09/10/157,076
CURRENT FILING DATE: 1999-11-24
PRIOR PLILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-25
   ö
  ö
   Sequence 7, Application US/09447800

| Sequence 7, Application US/09447800
| Patent No. 6537965
| GENERAL INFORMATION:
| APPLICANT: BRINGHURST, F. RICHARD
| APPLICANT: TAKASU, HISASHI
| APPLICANT: GARDELLA, THOMAS J.
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| CURRENT PILLING DATE: 1999-11-25
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PATENTIN VEY: 2.1
| SEQ ID NO 7
| TENGTH: 27
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  Length 27;
  Length 27;
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  0; Indels
   Score 59; DB 2;
Pred. No. 0.02;
  Score 59; DB 2;
Pred. No. 0.02;
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100.0%; Pred. No. vo...
0; Mismatches
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CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: 60/109,938
EARLIER FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 9
LENGTH: 27
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0; 7
  US-10-157-076-5; Sequence 5, Application US/10157076; Patent No. 6803213; GENERAL INFORMATION:
  LOCATION: (1) CTHER INFORMATION: Desamino Ala US-09-447-800-7
   Query Match 71.1
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Matches 12; Conservative
  1 AVSEIQLMHNLG 12
   Conservative
   1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
   TYPE: PRT
ORGANISM: Homo sapiens
  TYPE: PRT
CORGANISM: Homo sapiens
US-09-448-867-9
   Query Match
Best Local Similarity
Matches 12; Conserva<sup>(</sup>
   NAME/KEY: MOD_RES
  RESULT 6
US-09-447-800-7
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Gaps

seq-new.rai

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RESULT 13
US-09-843-221A-48
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   Query Match 71.1%; Score 59; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 12; Conservative 0; Mismatches 0; Indels
   Query Match 71.1%; Score 59; DB 2; Length 30; Best Local Similarity 100.0%; Pred. No. 0.023; Matches 12; Conservative 0; Mismatches 0; Indels
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1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
   TYPE: PRT
CRGANISM: Homo sapiens
US-10-157-076-8
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   US-10-15-016-0

Sequence 4, Application US/10157076

Patent No. 6603213

SEGENRAL INFORMATION:

APPLICANT: Bringhurst, F. Richard

APPLICANT: Takabu, Hisashi,

APPLICANT: Cardella, Thomas J.

APPLICANT: Potts, John T. Jr.

TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use

FILE REFERENCE: 0609.4440002

CURRENT APPLICATION NUMBER: US/10/157,076

CURRENT APPLICATION NUMBER: US 09/448,867

PRIOR FILING DATE: 1999-11-24

PRIOR FILING DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NOS: 13

SEQ ID NO 4

SEQ ID NO 6

  US-09-448-867-8

i Sequence 8, Application US/09448867

i Patent No. 6417333

i GENERAL INFORMATION:

APPLICANT: BINGHUEST, F. RICHARD

APPLICANT: TAKASU, HISASH

APPLICANT: GARDELLA, THOMAS J

APPLICANT: GARDELLA, THOMAS J

APPLICANT: POTTS JR. JOHN T.

ITILE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

ITILE OF INVENTION: AND USE

FILE REPERENCE: 0699.464000.

CURRENT APPLICATION NUMBER: US/09/448,867

CURRENT FILING DATE: 1999-11-24

EARLIER APPLICATION NUMBER: 60/109,938

EARLIER PILING DATE: 1998-11-25

NUMBER OF SEQ ID NOS: 13

SECTUARE PATENTING PATE: 1998-11-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO S: 13

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  Query Match 71.1%; Score 59; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 12; Conservative 0; Mismatches 0; Indels
  Query Match 71.1%; Score 59; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0
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GRGANISM: Homo sapiens
US-09-448-867-8
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US-10-157-076-4
US-09-448-867-4
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                     Sequence 6, Application US/09447800
; Sequence 6, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE
; CURRENT PLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-25
; BARLIER PLING DATE: 1998-11-25
; SEQ ID NO 6
; SEQ ID NO 6
; SEQ ID NO 6
; LINGTH: 33
  Gaps
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   71.1%; Score 59; DB 2; Length 33; 100.0%; Pred. No. 0.025; cive 0; Mismatches 0; Indels
   Sequence 3, Application US/08488105
; Sequence 3, Application US/08488105
; Patent No. 5717662
; GENERAL INFORMATION:
; APPLICANT: Chorev, Michael
; APPLICANT: Chorev, Michael
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Eish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
  STATE: MA
COUNTRY: USA
COMPUTER: USA
ZIP: TO10-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT NELSABLE TON UNBER: US/08/488,105
FILING DATE: 07-JUN-1995
CLASSFECATION UNBER: US/08/488,105
FILING DATE: 07-JUN-1995
CLASSFECATION NUMBER: 34,053
REGISTRATION NUMBER: 00537/112001
TELECOMMUNICATION NUMBER: 00537/112001
  NAME/KEY: MOD_RES
LOCATION: (1)
CTHER INFORMATION: Desamino Ala
US-09-447-800-6
   Query Match 71.1
Best Local Similarity 100.
Matches 12; Conservative
   1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
   TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                   JS-09-447-800-6
  US-08-488-105-3
  RESULT 16
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   /product= "OTHER"
/note= "This C-terminal amino acid is an amide, i.e., CONH2.'
   /product= "OTHER"
/note= "The side chains of Lys at position 18 and Asp at
position 22 are linked by an amide bond. "
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   Sequence 31, Application US/09228990
; Sequence 31, Application US/09228990
; Patent No. 6472505
; GENERAL INFORMATION:
    APPLICANT: Morize, Isabelle
    TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
    TUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Rhone-Poulenc Rorer Inc.
    STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
  71.1%; Score 59; DB 2; Length 31; 92.3%; Pred. No. 0.023; ive 0; Mismatches 1; Indel8
  ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PREMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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  LOCATION: 8 / OTHER INFORMATION: /product= "Nle"
   MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
   1 AVSEIQLXHNLGG 13
   1 AVSEIQLMHNLGG 13
  TOPOLOGY: not relevant
  Query Match 71.1
Best Local Similarity 92.3
Matches 12, Conservative
LOCATION: 18.22
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
THER INFORMATION:
NAME/KEX: Peptide
LOCATION: 31
  LOCATION: 31
OTHER INFORMATION:
OTHER INFORMATION:
   NAME/KEY: Peptide
   FEATURE:
NAME/KEY: Peptide
   USA
   STRANDEDNESS:
  FILING DATE:
  US-09-228-990-31
  RESULT 14
US-09-228-990-31
   COUNTRY:
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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  1 AVSEIQLMHNLG 12
   MOLECULE TYPE: protein
  Boston
   RESULT 18
US-08-488-105-15
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   셤
TOPOLOGY: linear

MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: The side chains of Lys at
OTHER INFORMATION: position 13 and Asp at postion 17 are linked by an amide bond
OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), rath
US-08-488-105-3
  OTHER INFORMATION: The side chains of Lys at OTHER INFORMATION: position 26 and Asp at position 30 are linked by an amide bor OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), rath OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
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  Gaps
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  Ouery Match 71.1%; Score 59; DB 1; Length 34; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 12; Conservative 0; Mismatches 0; Indels
  / Match 71.1%; Score 59; DB 1; Length 34; Local Similarity 100.0%; Pred. No. 0.026; Local Similarity 0.00%; Pred. No. 10.000 0
  Sequence 9, Application US/08488105
| Patent No. 5717062
| GENERAL INFORMATION:
| APPLICANT: Chorev, Michael
| APPLICANT: Chorev, Michael
| TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHEP
| VUMBER OF SEQUENCES: 22
| CORRESPONDENCES: 22
| CORRESPONDENCES: FADRESS:
| STREET: 225 Franklin Street
| STATE: MA
  COUNTY: USA
COMPUTER: USA
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TAN FC compatible
COMPUTER: TAN FC COMPATION: NO FELLO 
  LENGIN: ...
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
   TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 34 anino acids
  1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
   1 AVSEIQLMHNLG 12
  1 AVSEIQLMHNLG 12
   MOLECULE TYPE: protein
   US-08-488-105-9
  Query Match
   Best Loc
Matches
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CTHER INFORMATION: The side chains of Ly8 at CTHER INFORMATION: position 13 and Asp at position 17 and the side chains of Ly8 of OTHER INFORMATION: position 26 and Asp at position 30 are linked byy an amide bor cother information: and this sequence has an amide C-terminus (i.e., COOH).
   ..
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   Gaps
  US-09-447-800-5
US-09-447-800-5
Sequence 5, Application US/09447800
Patent No. 6537965
GENERAL INFORMATION:
APPLICANT: PRINGHURZT, F. RICHARD
APPLICANT: TAKASU, HISASHI
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
CURRENT APPLICATION NUMBER: US/09/447,800
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/110,152
EARLIER PILING DATE: 1998-11-25
   Ouery Match 71.1%; Score 59; DB 1; Length 34; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 12; Conservative 0; Mismatches 0; Indels
  STATE: MA

COUNTRY: USA

ZIP: 0210-2804

CONDITOR: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,105
FLIANG DATE: 07-UWA-1995
CLASSIPICATION: 530
ATTORNEY FAGBNT INFORMATION:
REGISTRATION NUMBER: 00537/112001
TELEPRATION NUMBER: 00537/112001
TELEPRATION NUMBER: 00537/112001
TELEPRATION NUMBER: 01/542-8906
TELEPRATION NUMBER: 01/542-8076
TELEPRATION NUMBER: 01/542-8076
TELEPRATION: 41/542-8076
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SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TUTOR OF SEQ ID NO: 15:
ELENGTH: 34 amino acids
Sequence 15, Application US/08488105
Patent No. 5717062
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chorev, Michael
TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHEP
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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```
RESULT 20
US-09-843-221A-25
i Sequence 25, Application US/09843221A
patent No. 6756480
i GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHIAN-FA
APPLICANT: LIU, CHIAN-FA
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID FILE REFERENCE: A-6658
CURRENT APPLICATION NUMBER: US/09/443,221A
CURRENT FILING DATE: 2001-04-26
FRIOR PILING DATE: 2001-02-06
FRIOR PILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 34
TYPE: RRI
SEC DATE: ACCURENT FAILURE
SEC DATE: 2000-04-27
SOFTWARE: PATENTE DATE: 2000
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US-10-192-673-5

Sequence 5, Application US/10192673

Sequence 5, Application No. US20030166838A1

GENERAL INFORMATION:

APPLICANT: Gardella, Thomas J.

APPLICANT: Brackella, John T.

APPLICANT: Harald

TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Hormone-Related Peptide (PTH) and Parathyroid

TITLE OF INVENTION: Hormone-Related Peptide (PTHP)

FILE REFERENCE: 0609-457002

CURRENT FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: US. 09/421,379

PRIOR APPLICATION NUMBER: US. 09/421,379

PRIOR APPLICATION NUMBER: US. 09/421,379

PRIOR APPLICATION NUMBER: US. 00/105,530

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 13

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LENGTH: 14

TYPE: PRT
APPLICANT: Hutchison, James Scott
TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
FILE REFERENCE: A1713
CURRENT APPLICATION NUMBER: US/09/898,398
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
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Squence 3, Application US/10921368

Publication No. US20050003493A1

GENERAL INFORMATION:

APPLICANT: Hutchison, James Scott

TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS

TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS

CURRENT FILE REPERBUCE: A1713

CURRENT FILE 2004-08-18

NUMBER OF SEQ ID NOS: 8

SOFUMARE: Patentin version 3.1

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US-09-730174A-5

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Sequence 5, Application US/09730174A

Patent No. US202020110871A1

Patent No. US202020110871A1

PAPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Ablective Binding Specificity to Bioactive Intact Parathyroid HC CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT APPLICATION NUMBER: US/09/730,174A

NUMBER OF SEQ ID NOS: 12

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| GENERAL INFORMATION:
| APPLICANT: Zahradnik, Richard J. |
| APPLICANT: Zahradnik, Richard J. |
| TITLE OF INVENTION: Actibodies and Peptide Antigens for Producing Antibodies having |
| TITLE OF INVENTION: Actibodies End Peptide Antigens for Producing Antibodies having |
| TITLE OF INVENTION: Hormone (PTH) 1-84 |
| FILE REFERENCE: INVENTE ON HORMER: US 09/730, 174 |
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| PRIOR PILING DATE: 2000-11-29 |
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US-10-998-927-5
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Publication No. US20030144209A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT TARASU, HISASHI
APPLICANT TARASU, HONORESI
CURRENT APPLICATION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE
CURRENT APPLICATION NUMBER: 05/10/361,928
CURRENT FILING DATE: 1099-11-23
PRIOR APPLICATION NUMBER: 60/110,152
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PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 10
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i Sequence 18 Application US/10484080

j Publication No. US20050026839A1

j GENERAL INFORMATION:
    APPLICANT Cardella, Thomas J.
    TITLE OF INVENTION: Conformationally Constrained Parathyroid
    TITLE OF INVENTION: Conformation (PTH) Analoge
    FILE REFERENCE: 0609-5110002

CURRENT FILING DATE: 2004-01-16

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 31

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SEOFTWARE: ALING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 31

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  APPLICANT: Zahradnik, R.J.
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HC FILE REFERENCE: IMUNE-001A CURRENT APPLICATION NUMBER: US/09/730,174A CURRENT FILING DATE: 2000-12-05 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 11
LENGTH: 15
   APPLICANT: Lavigne, Jeffrey R.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid TITLE OF INVENTION: Hormone (PTH) 1-84
FILE REPERENCE: IMUNE-001B
CURRENT APPLICATION NUMBER: US/10/998,927
CURRENT FILING DATE: 2004-11-29
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APPLICANT: Zahradnik, Richard J.
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Publication No. US20050203012A1
GENERAL INFORMATION:
APPLICANT: Bringhurst, F. Richard
APPLICANT: Takasu, Hisashi
APPLICANT: Takasu, Hisashi
APPLICANT: Gardella, Thomas J.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
TITLE OF INVENTION: and Use
FILE REPERRNCE: 0609-4640002
CURRENT FILING DATE: 2002-05-30
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FRICK PILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-25
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(APPLICANT: Tarkau: Hissahi
(APPLICANT: Potts, John T. Jr.
(APPLICANT: Potts, John T. Jr.
(APPLICANT: Bringhurer: US-009-4640002 8.000
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Sequence 8, Application US/10959605

Publication No. US20050203012A1

GENERAL INFORMATION:

APPLICANT: Bringhurst, F. Richard

APPLICANT: Takasu, Hissahi

APPLICANT: Takasu, Hissahi

APPLICANT: Takasu, Hissahi

APPLICANT: Gardella, Thomas J.

TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

TITLE OF INVENTION: Bund Use

TITLE OF INVENTION: WIMBER: US/10/959,605

CURRENT APPLICATION NUMBER: US/10/157,076

PRIOR APPLICATION NUMBER: US 69/448,867

PRIOR APPLICATION NUMBER: US 60/109,938

PRIOR FILING DATE: 1998-11-25

NUMBER OF SEQ ID NOS: 13

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SEQ ID NO 8

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TENTINE DATE: 1998-11-25
APPLICANT: Takagu, Hisashi
APPLICANT: Takagu, Hisashi
APPLICANT: Takagu, Hisashi
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
TITLE OF INVENTION: and Use
FILE REPERENCE: 0609-4640002,
CURRENT APPLICATION NUMBER: US/10/959,605
CURRENT APPLICATION NUMBER: US/10/157,076
FRIOR APPLICATION NUMBER: US 09/448,867
FRIOR APPLICATION NUMBER: US 09/448,867
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Publication No. US20040176568A1

GENERAL INFORMATION:

APPLICANT: Bringhurst, F. Richard

APPLICANT: Bringhurst, F. Richard

APPLICANT: Takasu, Hisashi

APPLICANT: Potts, John T. Jr.

TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use

FILE REFERENCE: 0609 4640002

CURRENT APPLICATION NUMBER: US/10/157, 076

CURRENT FILING DATE: 12999-11-24

PRIOR APPLICATION NUMBER: US 60/448,867

PRIOR APPLICATION NUMBER: US 60/109,938

PRIOR FILING DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

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APPLICANT: Takasu, Thomas J.
APPLICANT: Takasu, Thomas J.
APPLICANT: Takasu, Thomas J.
APPLICANT: Potts, John T. Jr.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
TILE REFRENCE: 0609.4640002
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Sequence 48, Application US/09999608
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Publication No. US20050124537A1
SEQUENCE THORMWAITON:
APPLICANT: GOSTENUIK, PAUL
APPLICANT: KINSTLER, CLAF BORIS
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: MODBER: US/09/999, 608
TITLE OF INVENTION: WORDER: US/09/999, 608
FRICH APPLICATION NUMBER: US 09/843,221
FRICH APPLICATION NUMBER: US 60/266,673
FRICH PRILING DATE: 2000-06-28
FRICH RELING DATE: 2000-06-28
FRICH RELING DATE: 2000-06-28
FRICH RELING DATE: 2000-06-27
NUMBER OF SEC ID NOS: 193
SEC ID NO 48
APPLICANT: KOSTENUIK, PAUL

APPLICANT: LLU, CHUANF FA

APPLICANT: LLU, CHUANF FA

APPLICANT: LLU, CHUANF FA

APPLICANT: LLU, CHUANF FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H

FILE REFERENCE: A-665B

CURRENT APPLICATION NUMBER: US/09/843,221A

CURRENT APPLICATION NUMBER: 60/266,673

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE PATENTION NUMBER: 60/200,053

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 48

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US-09-999-608-48
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GENERAL INTEGRALIANTE ROSTENDIK, PAUL
APPLICANT: LOW CHUNAN-FA
TITLE OF INVENTION: MEDIATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/943,221A
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2001-02-06
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PRIOR FILING DATE: 2000-06-28
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71.1%; Score 59; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.14;
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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

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US-10-939-890-826

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US-10-939-890-752

US-10-939-890-722

US-10-939-890-721

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-939-890-351
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Maximum Match 100%
Listing first 100 summaries
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   score greater than or equal to and is derived by analysis of t
   length: 0
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Maximum DB seq
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Sequence Sequence Sequence

Sequence Sequence Sequence

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US-10-939-890-382 US-10-939-890-385

US-10-939-890-698 US-10-939-890-701 US-10-939-890-820 US-10-939-890-821

US-10-467-962B-83 US-10-967-457-79 US-10-841-129-7

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US-11-109-156-16 US-10-131-826A-340 US-10-984-376-2

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1 LOCATION: (28]...(28)

1 COTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

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  APPLICANT: POLLUL, SLYLL
APPLICANT: POLLUL, SLYLL
APPLICANT: Shadlingam, Kondareddiar
APPLICANT: Shadlingam, Kondareddiar
APPLICANT: Song, Song, Song, Song, Song, Song, Rorleant: Song, Mathew A.
APPLICANT: Won Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGFKOR BINDING PEPTIDES
FILE REPERENCE: D0617, 70014U500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/931,082
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: PG7/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-01
  RESULT 3
US-10-393-890-723
is Sequence 723, Application US/10939890
is General INPORMATION:
GENERAL INPORMATION:
APPLICANT: Sexton, Daniel J.
APPLICANT: Sexton, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
  OTHER INFORMATION: Synthetic peptide
   Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
  Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Num, Adrian D.
Arbogast, Christophe
Busat, Philippe
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
  LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
  TYPE: PRT
ORGANISM: Artificial sequence
  3 SEIQLMHNLGGGGG 16
   14 ADLQLSHFAGGGG 27
   NAME/KEY: MOD RES
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0
          Sequence 6, Appli
Sequence 334, App
  Gaps
  ;
0
   Query Match 56.6%; Score 47; DB 1; Length 28; Best Local Similarity 57.1%; Pred. No. 0.02; Matches 8; Conservative 3; Mismatches 3; Indels
  APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: NOR AND VEGFKEDR BINDING PEPTIDES
FILE REFERENCE: D6617, 70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
      1 US-10-967-648A-6
7 US-11-082-389-334
  PRIOR APPLICATION NUMBER: US/10/939,890
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR PLILNG DATE: 2003-09-11
PRIOR PLILNG DATE: 2003-09-01
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 0/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PLILNG DATE: 2003-03-03
PRIOR PLILNG DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
NUMBER OP SEQ ID NOS: 883
SOFTWARE: PERIORS FOR WINDOWS VERSION 4.0
SEQ ID NO 464
LENGTH: 28
   ALIGNMENTS
   Sequence 464, Application US/10939800
| Sequence 464, Application US/10939800
| Publication No. US20050250700A1
| GENERAL INFORMATION:
| APPLICANT: Sexton, Daniel J.
| APPLICANT: Dransfield, Daniel T.
| APPLICANT: Ladner, Robert C.
| APPLICANT: Ladner, Robert C.
| APPLICANT: Pan, Hong APPLICANT: Pan, Hong APPLICANT: Pan, Hong APPLICANT: Pan, Hong APPLICANT: Marinelli, Edmund R.
| APPLICANT: Marinelli, Radnariappa APPLICANT: Pillai, Radhakrishna APPLICANT: Pochon, Sibylle APPLICANT: Ramalingam, Kondareddiar APPLICANT: Ramalingam, Kondareddiar APPLICANT: Ramalingam, Kondareddiar APPLICANT: Ramalingam, Ajay
  RESULT 2
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(S-10-939-90-720)
(Sequence 720, Application US/10939890)
(Publication No. US20050250700A1)
(GNERAL INFORMATION:
(APPLICANT: Sato, Aaron K.)
(APPLICANT: Sexton, Daniel J.)
(APPLICANT: Ladner, Robert C.)
   ; OTHER INFORMATION: Library Isolate US-10-939-890-464
  TYPE: PRT ORGANISM: Artificial Sequence
   3 SEIQLMHNLGGGGG 16
  14 ADLQLSHFAGGGGG 27
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Gaps

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; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide US-10-939-890-353
  53.0%; Score 44; DB 1; Length 28; 70.0%; Pred. No. 0.057; tive 1; Mismatches 2; Indels
   APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, wathew A.
TITLE CO INVENTION: ROL AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/10/930,890
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PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US/06/40,411
PRIOR PILING DATE: 2003-01-15
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PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2004-09-13
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PRIOR PILING DATE: 2003-03-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01
SEQUENARE: PSECSE FOR WINDOWS VETSION 4.0
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  Sequence 829, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
   Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
  APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
  Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
   TYPE: PRT ORGANISM: Artificial Sequence
  Shrivastava, Ajay
   Nunn, Adrian D.
   Query Match 53.0
Best Local Similarity 70.0
Matches 7; Conservative
  7 LMHNLGGGGG 16
   18 MFHQLGGGG 27
  IS-10-939-890-829
   FEATURE:
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   Gaps
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   Query Match 56.6%; Score 47; DB 1; Length 28; Best Local Similarity 57.1%; Pred. No. 0.02; Matches 8; Conservative 3; Mismatches 3; Indels
   NAME/KEY: MOD RES
LOCATION: (28)
COTHER INFORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723
   APPLICANT: STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT SONG, BO APPLICANT: SWENGON, ROLF E. APPLICANT: SWENGON, ROLF E. APPLICANT: SWENGON, ROLF E. APPLICANT: SWENGON, ROLF E. STATEMENT SWENGON, ROLF AND VEGF/KDR BINDING PEPTIDES FILE REFERENCE: DG617.700140500 CURRENT APPLICATION NUMBER: US 10/939,890 CURRENT FILING DATE: 2004-09-13 PRIOR FILING DATE: 2004-09-13 PRIOR FILING DATE: 2003-09-11 PRIOR PELICATION NUMBER: US 10/382,082 PRIOR PELICATION NUMBER: US 60/440,411 PRIOR PELICATION NUMBER: US 60/440,411 PRIOR FILING DATE: 2003-01-15 PRIOR PELICATION NUMBER: US 60/360,851 PRIOR FILING DATE: 2003-01-15 PRIOR PELICATION NUMBER: US 60/300,851 PRIOR FILING DATE: 2003-01-15 PRIOR PELICATION NUMBER: US 60/300,851 PRIOR PERIOR PERIOR PELICATION NUMBER: US 60/300,851 PRIOR PELICATION NUMBER: US 60/300,851 PRIOR PELICATION NUMBER: US 60/300,851 PRIOR PERIOR PERIO
  APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
   Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
   OTHER INFORMATION: Synthetic peptide
  Sequence 353, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
  APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Fan, Hong APPLICANT: Khurana, Sudha APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
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   LOCATION: (1). (1)
OTHER INFORMATION: ACETYLATION
  TYPE: PRT
ORGANISM: Artificial sequence
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  3 SEIOLMHNLGGGGG 16
   Song, Bo
Swenson, Rolf E.
  FEATURE:
NAME/KEY: MOD_RES
   US-10-939-890-353
  LOCATION:
  FEATURE:
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Gaps

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2; Indels

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Best Local Similarity 53.8%; Pred. No. 0.11;
Matches 7; Conservative 4; Mismatches
   Sequence 830, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arboqast, Christophe
APPLICANT: Bussat, Philippe
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  |::|: |||||
14 EVELVDHPGGGGG 26
   FEATURE:
NAME/KEY: MOD RES
LOCATION: (27)..(2
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  Gaps
  NAME/KEY: MOD RES

) LOCATION: (28)

) OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-829
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  ; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide US-10-939-890-354
   Query Match 53.0%; Score 44; DB 1; Length 28; Best Local Similarity 70.0%; Pred. No. 0.057; Matches 7; Conservative 1; Mismatches 2; Indels
  APPLICANT: Song, Bo
APPLICANT: Senson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: DG617.70014U0500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
  PRIOR APPLICATION DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-09-13
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03-03
PRIOR PILING DATE: 2003-03-03-03
PRIOR PRILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PRECECT WINDOWS Version 4.0
  Fan, Hong
Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
   FEATURE:
OTHER INFORMATION: Synthetic peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
  Sequence 354, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
   APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Lidner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                          TYPE: PRT
ORGANISM: Artificial sequence
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18 MFHQLGGGGG 27
   7 LMHNLGGGGG 16
  LENGTH: 28
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   Query Match 50.6%; Score 42; DB 1; Length 27; Best Local Similarity 53.8%; Pred. No. 0.11; Matches 7; Conservative 4; Mismatches 2; Indels
  APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Own Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGFKDR BINDING PEPTIDES
TITLE OF INVENTION: KDR AND VEGFKDR BINDING PEPTIDES
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/392,082
PRIOR APPLICATION NUMBER: US 00/40,111
PRIOR APPLICATION NUMBER: CO.
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
   INFORMATION: Synthetic peptide
  NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
   TYPE: PRT
ORGANISM: Artificial sequence
   4 EIQLMHNLGGGGG 16
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14 EVELVDHPGGGGG 26
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50.6%; Score 42; DB 1; Length 27;

Query Match

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Query Match
45.8%; Score 38; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.48;
Matches 7; Conservative 1; Mismatches 2; Indels
  APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.7001410SO
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
   APPLICANT: SWENGON, MOLI E.
APPLICANT: SWENGON, MOLI E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.70014U500
CURRENT FILING DATE: 2004-09-13
FRIOR PPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2003-09-11
FRIOR PILING DATE: 2003-09-11
FRIOR APPLICATION NUMBER: US 10/861,156
FRIOR APPLICATION NUMBER: US 10/803/06731
FRIOR APPLICATION NUMBER: PCT/US03/06731
FRIOR FILING DATE: 2003-03-03
FRIOR FILING DATE: 2003-01-15
FRIOR APPLICATION NUMBER: US 60/440,411
FRIOR FILING DATE: 2002-01-15
FRIOR FILING DATE: 2002-03-01
  Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
  Sequence 699, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
   CTHER INFORMATION: Library Isolate US-10-939-890-383
  APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Busaat, Philippe
  ORGANISM: Artificial Sequence
   Song, Bo
Swenson, Rolf E.
   7 LMHNLGGGGG 16
   | |: |||||
18 LNHSPGGGGG 27
  Song, Bo
   JS-10-939-890-699
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   Gaps
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  ; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide US-10-939-890-346
  Query Match 45.8%; Score 38; DB 1; Length 28; Best Local Similarity 70.0%; Pred. No. 0.48; Matches 7; Conservative 1; Mismatches 2; Indels
   APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Won Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: DOG17.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PLICATION NUMBER: PCT/US03/06731
PRIOR PLICATION NUMBER: US 60/440,411
PRIOR PLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR PLING DATE: 2003-01-15
PRIOR PLING DATE: 2003-03-01
PRIOR FILING DATE: 2003-03-01
PRIOR FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 346
  APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Pochon, Sibylle
APPLICANT: Pochon, Sibylle
APPLICANT: Sanalingam, Kondareddiar
PPLICANT: Song, Bo
PPLICANT: Song, Bo
   Sequence 383, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
  ; Sequence 346, Application US/10939890; Publication No. US20050250700A1; GENERAL INFORMATION:
   APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Pansat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Linder, Karen E.
APPLICANT: Manjappan, Palaniappa
  TYPE: PRT
ORGANISM: Artificial Sequence
  7 LMHNLGGGGG 16
   | |: |||||
18 LNHSPGGGGG 27
   US-10-939-890-383
  FEATURE:
   셤
   8
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Gaps

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RESULT 12
US-10-972-587-37
US-10-972-587-37
Sequence 37, Application US/10972587
Fublication No. US20050246799A1
GENERAL INFORMATION:
APPLICANT: Bariola, Pauline Anne
APPLICANT: Bariola, Pauline Anne
APPLICANT: Linderoth, Nora Abiella
APPLICANT: Wei, Zhong-Min
APPLICANT: Wei, Shong-Min
APPLICANT: Wei, Shong-Min
APPLICANT: Linderoth, Nora Baicle
CURRENT FILING DATE: 2004-10-25
FRIOR APPLICATION NUMBER: 60/35,776
FRIOR APPLICATION NUMBER: 09/810,997
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-06-17
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin Ver: 2.1
FENCH: 114
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  Gaps
  FEATURE:
NAME/KEX: MD. RES
LOCATION: (9). (9)
PETURE:
PEATURE:
PEATURE:
NAME/KEX: MOD. RES
LOCATION: (2). (2)
OTHER INFORMATION: Lys residue modified with a iv-bde linker
PEATURE:
COTHUR:
NAME/KEX: MOD. RES
LOCATION: (28)
COTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-822
  Query Match
Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 2; Indels 3
  Query Match

45.8%; Score 38; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.48;
Matches 7; Conservative 1; Mismatches 2; Indels
  ; ORGANISM: Xanthomonas campestris pv. pelargonii
US-10-972-587-37
  CONTREE INFORMATION: Synthetic peptide FRATURE: NAME/KEY: MOD RES LOCATION: (1) (1) OCHER INFORMATION: ACETYLATION
   RESULT 13
105-10-399-890-700
105-10-399-890-700
105-10-399-890
105-10-399-890-700
105-10-399-890
105-10-399-890-700
105-10-399-890-700
105-10-399-890-700
105-10-399-890-700
105-10-399-890-700
105-10-399-890-700
105-10-39
  TYPE: PRT ORGANISM: Artificial sequence
  89 MOLMONOGGAGMGGG 103
  7 LIMHNLGGGGG 16
   18 LNHSPGGGGG 27
  ò
   ö
   NAME/KEY: MOD_RES

1 LOCATION: (28)

OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-699
   Gaps
  Query Match 45.8%; Score 38; DB 1; Length 28; Best Local Similarity 70.0%; Pred. No. 0.48; Matches 7; Conservative 1; Mismatches 2; Indels
  APPLICANT: SONG; HO
APPLICANT: SONG; HO
APPLICANT: SONG; HO
APPLICANT: VON WRONSKI, MATHEW A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERBENCE: DOG17:70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-13
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR PILING DATE: 2003-09-13
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FRASESQ FOR WINDOWS VERSION 4.0
PRIOR APPLICATION NUMBER: PCT/USO3/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FREESEQ for Windows Version 4.0
EDGTH: 28
   APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Bransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Arbogast, Christophe
APPLICANT: Far, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Manjappan, Ralaniappa
APPLICANT: Manjappan, Palaniappa
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nanjappan, Ralaniappa
APPLICANT: Pillai, Radhakrishna
APPLICANT: Sohon, Sibylle
APPLICANT: Shrivagtava, Ajay
APPLICANT: Song, 80
  OTHER INFORMATION: Synthetic peptide
  Sequence 822, Application US/10939890; Publication No. US20050250700A1; GENERAL INFORMATION:
  FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
   TYPE: PRT ORGANISM: Artificial sequence
   18 LNHSPGGGGG 27
   7 LMHNLGGGGG 16
   RESULT 11
US-10-939-890-822
```

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APPLICANT: APPLICANT: APPLICANT:

APPLICANT APPLICANT

APPLICANT

```
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Lavalie, Edward R
APPLICANT: Lavalie, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Peace, Muscice
APPLICANT: Treacy, Muscice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION NUMBER: US/10/689,742
CURRENT FILING DATE: 2000-12-21
PRIOR PAPLICATION NUMBER: 09/746,783
PRIOR PAPLICATION NUMBER: 09/746,783
PRIOR PAPLICATION NUMBER: 09/746,783
PRIOR PAPLING DATE: 2000-12-21
NUMBER OF SEC ID NOS: 231
SOFTWARE: PARCENTIN version 3.2
SOFTWARE: PARCENTIN version 3.2
  Gaps
  ö
   Query Match 44.6%; Score 37; DB 1; Length 28; Best Local Similarity 85.7%; Pred. No. 0.68; Matches 6; Conservative 1; Mismatches 0; Indels
   APPLICANT: Nunn, Adrian D.
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radharishna
APPLICANT: Pochon, Sibyle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shivastava, Ajay
APPLICANT: Swenson, Rolf E.
APPLICANT: Won Wronski, Mathew A.
TITLE REFERENCE: D0617, 700140500
CURRENT APPLICATION NUMBER: US 10/661,156
FRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-01-15
PRIOR APPLICATION NUMBER: US 60/460,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
SEQ ID NOS: 883
SOFTWARE: PastSEQ for Windows Version 4.0
   Sequence 100, Application US/10689742
Publication No. US20050250180A1
GENERAL INFORMATION:
  , OTHER INFORMATION: Library Isolate US-10-939-890-384
Marinelli, Edmund R.
Nanjappan, Palaniappa
  ORGANISM: Artificial Sequence
   TYPE: PRT
CORGANISM: Homo sapiens
US-10-689-742-100
   10 NLGGGGG 16
   21 NVGGGGG 27
  US-10-689-742-100
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  NAME/KEY: MOD_RES

LOCATION: (27)..(27)

OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-700
   Gaps
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0
   44.6%; Score 37; DB 1; Length 27;
85.7%; Pred. No. 0.65;
tive 1; Mismatches 0; Indels
  APPLICANT: SULTANT: SULTANT: SULTANT: SURGES BOOK BOOK BOLTANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: VON WEONSKI, Mathew A.
TITLE OF INVENTION: NEW AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014USO
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR PLING DATE: 2003-01-15
   Sexton, Daniel J.
Dransfield, Daniel T.
Ladner, Robert C.
Arbogaet, Christophe
Bussat, Philippe
Khurana, Sudha
Linder, Karen E.
Marinelll, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
  OTHER INFORMATION: Synthetic peptide
   ; Sequence 384, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
  APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
  LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
   TYPE: PRT
ORGANISM: Artificial sequence
   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
   10 NLGGGGG 16
   |:|||||
20 NVGGGGG 26
  NAME/KEY: MOD_RES
   US-10-939-890-384
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FEATURE:

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Query Match

44.6%; Score 37; DB 1; Length 368;

Best Local Similarity 53.8%; Pred. No. 9.7;

Matches 7; Conservative 2; Mismatches 4; Indels

Fan, Hong Khurana, Sudha Linder, Karen E.

APPLICANT: APPLICANT:

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Sequence 9, Application US/11013759;
Sequence 9, Application US/11013759;
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: LOSEMORE, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Arang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: 1038-921MIS: jb
CURRENT FILING DATE: 1038-921MIS: jb
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
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SEQ ID NOS: 32
SEQ ID NOS: 32
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REPERBRUE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: 02/04/11/013,759
PRIOR APPLICATION NUMBER: 05/09/361,619
PRIOR PELLING DATE: 1099-07-27
SOFTWARE: PALENT NOS: 32
SOFTWARE: PALENT NOS: 21
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  Score 35; DB 7; Length 2047; Pred. No. 1.2e+02; 2; Mismatches 5; Indels
  US-10-939-890-325
; Sequence 325, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sacto, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Busseat, Philippe
; APPLICANT: Khurana, Sudha
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
   ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-9
  ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-7
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Best Local Similarity 50.0%;
Matches 7; Conservative
   1 AVSEIQLMHNLGGG 14
  18 AVAEYAKSHSTGGG 31
   1 AVSEIQLMHNLGGG 14
   2047
   2053
  RESULT 19
US-11-013-759-9
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   Gaps
   NGS-11-169-013-2
Sequence 2, Application US/11169013
Sequence 2, Application Woll1169013
Fublication No. US20050244971A1
GENERAL INFORMATION:
APPLICANT: Korea Kunho Petrochemical Co., Ltd.
TILLE OF INVENTION: TRANSGENIC PLANTS WITH ENHANCED STRESS TOLERANCE:
CURRENT APPLICATION NUMBER: US/11/169,013
CURRENT FILING APIG. 2005-06-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Kopatentin 1.71
LENGTH: 431
   Query Match 42.2%; Score 35; DB 7; Length 2047; Best Local Similarity 50.0%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 5; Indels
  Score 35; DB 7; Length 431;
Pred. No. 23;
1; Mismatches 0; Indels
   Sequence 7, Application US/11013759; Publication No. US20050249747A1; GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M. APPLICANT: Sasaki, Ken
  ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-4
  ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-169-013-2
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Best Local Similarity 85.7%;
Matches 6; Conservative
   1 AVSEIQLMHNLGGG 14
  2 VSEIQLMHNLGGG 14
   9 HNLGGGG 15
  8 NNLGGGG 14
  RESULT 17
US-11-013-759-4
   US-11-013-759-7
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APPLICANT: Marinelli, Edwund R.
APPLICANT: Naniappan, Pataniappa
APPLICANT: Naniappan, Pataniappa
APPLICANT: Naniappan, Pataniappa
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Song, Bo
CURRENT APPLICANTON NUMBER: US/10/939,890
CURRENT APPLICANTON NUMBER: US/10/931,800
PRIOR APPLICANTON NUMBER: US 50/40,911
PRIOR APPLICANTON NUMBER: US 60/440,411
PRIOR APPLICANTON NUMBER: US 60/440,411
PRIOR PLING DATE: 2003-03-03
03
PRIOR PLING DATE: 2003-03-03
PRIOR DATE: 2003-03-03
PRIOR DATE: 2003-03-03
PRIOR DATE: 2003-03-03
PRIOR DATE: 20
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Search completed: November 21, 2005, 16:56:34 Job time : 6 secs

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